

GenCore version 5.1.6  
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### On protein - protein search, using SW model

Run on: January 6, 2005, 10:39:49 ; Search time 38 seconds  
(without alignments)  
25.320 Million cell updates/sec

Title: US-10-047-945-1  
Perfect score: 54  
Sequence: 1 LKAMDPPTPPL 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

**Database :** PIR\_79;\*  
1: pir1;\*  
2: pir2;\*  
3: pir3;\*  
4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Result No.	Score	Query Match Length	DB ID	Description	
1	27	50.0	A36454	trypsin-modulating lectin - potato (F	
2	24	44.4	S21288	usease (EC 3.5.1.5 peptide-N4-(N-acetyl	
3	21	38.9	C35589	major protein anti	
4	21	38.9	10 2	enamelin f - bovin	
5	20	37.0	B60272	T-cell receptor be	
6	20	37.0	5 2	exotoxin A - Strept	
7	19	35.2	S10783	collagen alpha 2(V	
8	19	35.2	9 2	T-cell receptor be	
9	19	35.2	A60108	metallothionein-A	
10	19	35.2	10 2	alcohol dehydrogen	
11	18	33.3	C35572	triacylglycerol 11	
12	18	33.3	15 049	hemetinin (EC 3.4.-	
13	18	33.3	S71919	alpha-gliadin 4Hα	
14	18	33.3	PC2171	lectin - potato (fragment)	
15	17	31.5	10 2	C321288	C.Species: Solanum tuberosum (potato)
16	17	31.5	A61218	C.Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004	
17	16	29.6	5 2	C.Accession: S21288	C.Species: Solanum tuberosum (potato)
18	16	29.6	D48866	C.Residues: 1-8 <MIL>	
19	16	29.6	9 4	C.Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.	
20	16	29.6	10 2	Biochem. J. 283, 813-821, 1992	
21	15	27.8	8 4	A.Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizati	
22	15	27.8	I54017	A.Reference number: S21288; MUID:92272633; PMID:1290771	
23	15	27.8	9 2	A.Accession: S21288	A.Molecule type: protein
24	15	27.8	S15850	A.Residues: 1-8 <MIL>	
25	15	27.8	B39517	A.Cross-references: UNIPROT:Q7M1V6	
26	15	27.8	9 4	A.Experimental source: var. Ulster Sceptre	
27	15	27.8	P05654	C.Function:	
28	15	27.8	10 2	A.Description: may be involved in defence mechanism of the plant	
29	15	27.8	S18396	Ig mu chain J regi	
	10 2	PX0330			
	10 2	F33932			

### ALIGNMENTS

RESULT 1	QY	5 DPTRPP 9	Db	2 DRPP 6
A36454				
trypsin-modulating oestatic factor - yellow fever mosquito				
C.Species: Aedes aegypti (Yellow fever mosquito)				
C.Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004				
C.Accession: A36454; A61650				
R.Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.				
RASB, J. 4, 301-302, 1990				
A.Title: Mosquito oestatic factor: a novel decapeptide modulating trypsin-like enzyme b.				
A.Reference number: A36454; MUID:9036788; PMID:2394318				
A.Molecule type: protein				
A.Residues: 1-10 <BOR>				
A.Cross-references: UNIPROT:PI19425				
R.Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.				
Insect Biochem. Mol. Biol. 23, 703-712, 1993				
A.Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oestatic factor.				
A.Reference number: A61630; MUID:93535794; PMID:8353526				
A.Accession: A61630				
A.Molecule type: protein				
A.Residues: 1-10 <BOZ>				
A.Note: none of the amino acids is modified				
A.C.Function:				
A.Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut e				
C.Keywords: hormone				
Query Match	50.0*	Score 27; DB 2; Length 10;		
Best Local Similarity	80.0*	Pred. No. 58; Mismatches		
Matches	4;	Conservative 0; Indels 1; Gaps 0;		
QY	5 DPTRPP 9			
Db	2 DRPP 6			

C;Keywords: hydroxyproline; lectin

Query Match Score 24; DB 2; Length 8;

Best Local Similarity 57.1%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 2;

Indels 0; Gaps 0;

Db 2 ASTPSPP 8

RESULT 3

C35389 urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)

C;Species: Morganella morganii

C;Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 09-Jul-2004

C;Accession: C35389

J. Bacteriol. 172, 3073-3080, 1990

A;Title: Morganella morganii urease: purification, characterization, and isolation of ge

A;Reference number: A35389; MUID:90264298; PMID:2345135

A;Accession: C35389

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-110 <HUA>

A;Cross-references: UNIPROT:P17339

C;Keywords: hydrolase

Query Match Score 21; DB 2; Length 10;

Best Local Similarity 39.9%; Pred. No. 6.6e+02;

Matches 4; Conservative 0; Mismatches 2;

Indels 0; Gaps 0;

Db 1 MQLTPP 6

RESULT 4

B59272 peptide-N4-(N-acetyl-beta-D-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain

C;Species: Prunus dulcis var. sativa (sweet almond)

C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 09-Jul-2004

C;Accession: B59272

R;Altmann, F.; Paechinger, K.; Dalki, T.; Vorauer, K.

Bur. J. Biochem. 252, 118-123, 1998

A;Title: Characterisation of peptide-N4-(N-acetyl-beta-D-glucosaminyl)asparagine amidase A

A;Reference number: A55272; MUID:8181894; PMID:523720

A;Accession: B59272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ALT>

A;Cross-references: UNIPROT:P81898

C;Keywords: hydrolase

Query Match Score 21; DB 2; Length 10;

Best Local Similarity 39.9%; Pred. No. 6.6e+02;

Matches 3; Conservative 1; Mismatches 0;

Indels 0; Gaps 0;

Db 5 DPTPP 8

RESULT 5

B60274 major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)

C;Species: Mycobacterium tuberculosis

C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993

C;Accession: B60274

R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the culture

A;Reference number: A60274; MUID:9109998; PMID:1898899

A;Accession: B60274

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <NAGG>

Query Match Score 20; DB 2; Length 5;

Best Local Similarity 37.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1;

Indels 0; Gaps 0;

Db 5 DPTP 8

RESULT 6

S10783 enamelin f - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998

C;Accession: S10783

R;Strawich, E.; Glimcher, M.J.

Eur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth enamelins identified mainly as serum proteins. Major 'enamelin' is albu

A;Reference number: S10780; MUID:90336641; PMID:2379503

A;Accession: S10783

A;Molecule type: protein

A;Residues: 1-8 <SRR>

C;Keywords: enamel; phosphoprotein

Query Match Score 20; DB 2; Length 8;

Best Local Similarity 37.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1;

Indels 0; Gaps 0;

Db 6 PTTP 9

RESULT 7

S30572 T-cell receptor beta chain C region (CRTB29) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1989 #sequence\_revision 03-Apr-1989 #text\_change 30-May-1997

C;Accession: C30572

R;Williams, C.B.; Gutman, G.A.

J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz

A;Reference number: A30563; MUID:89110038; PMID:2533271

A;Accession: B30572

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-9 <WIL>

C;Keywords: T-cell receptor

Query Match Score 19; DB 2; Length 9;

Best Local Similarity 35.2%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Db 7 TPP 9

RESULT 8

A60108 exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)

C;Species: Streptococcus pyogenes

C;Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 09-Jul-2004

C;Accession: A60108

R;Schlievert, P.M.; Gray, E.D.

Infect. Immun. 57, 1865-1867, 1989

A;Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blast  
A;Reference number: A60108; MUID:89254013; PMID:2498210  
A;Accession: A60108  
A;Molecule type: protein.  
A;Residues: 1-9 <SCH>  
A;Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNI  
C;Keywords: exotoxin

Query Match 35.2%; Score 19; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTP 8  
Db 2 DPP 5

RESULT 9  
S26508  
collagen alpha 2(VI) chain - bovine (fragment)  
C;Species: Bos primigenius taurinus (cattle)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S26508  
R;Jander, R.; Rautenberg, J.; Glanville, R.W.  
Bur. J. Biochem. 133, 39-46, 1983  
A;Title: Further characterization of the three polypeptide chains of bovine and human sh  
A;Reference number: S26506; MUID:83209648; PMID:6852033  
A;Accession: S26508  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <JAN>  
A;Cross-references: UNIPROT:Q7M2M9  
C;Keywords: hydroxyproline (Pro) #status experimental  
F;7/Modified site: hydroxyproline (Pro) #status experimental

Query Match 35.2%; Score 19; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 PTPP 9  
Db 4 PGPP 7

RESULT 10  
C30572  
T-cell receptor beta chain C region (CRTB49) - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Apr-1989 #sequence\_revision 03-Apr-1989 #text\_change 30-May-1997  
C;Accession: C30572  
R;Williams, C.B.; Gutman, G.A.  
J; Immunol. 142, 1027-1035, 1989  
A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz  
A;Reference number: A0563; MUID:8910038; PMID:2563271  
A;Accession: C30572  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-10 <WIL>  
C;Keywords: T-cell receptor

Query Match 35.2%; Score 19; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TPP 9  
Db 7 TPP 9

RESULT 11  
151049  
metallothionein-A - rainbow trout (fragment)  
C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C;Accession: I51049  
R;Olsson, P.E.; Kling, P.; Brkell, L.J.; Kille, P.  
Bur. J. Biochem. 230, 344-349, 1995  
A;Title: Structural and functional analysis of the rainbow trout (*Oncorhynchus mykiss*) m  
A;Reference number: I51049; MUID:95324545; PMID:7601121  
A;Sttus: preliminary; translated from GB/EMBL/DDJB  
A;Accession: I51049  
A;Molecule type: DNA  
A;Cross-references: EMBL:X80181; NID:gi1019799; PIDN:CAAS6466.1; PID:94379328  
A;Cross-references: UNIPROT:Q7M2M9  
C;Keywords: NAD; oxidoreductase  
A;Cross-references: UNIPROT:Q7I246  
A;Accession: S71919; MUID:96350418; PMID:8765227  
A;Title: Proteolytic activation of grass carp (*Ctenopharyngodon idellus*) liver alcohol d  
A;Reference number: S71919  
A;Accession: S71919  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <TSU>  
A;Cross-references: UNIPROT:Q7I246  
A;Note: the source is designated *Ctenopharyngodon idellus*  
C;Keywords: NAD; oxidoreductase

RESULT 12  
S71919  
alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)  
C;Species: *Ctenopharyngodon idellus* (grass carp)  
C;Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 09-Jul-2004  
C;Accession: S71919  
R;Tsui, H.T.; Mock, W.Y.; Lau, K.K.; Fong, W.P.  
Biochim. Biophys. Acta 1286, 41-46, 1996  
A;Title: Proteolytic activation of grass carp (*Ctenopharyngodon idellus*) liver alcohol d  
A;Reference number: S71919  
A;Accession: S71919  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <TSU>  
A;Cross-references: UNIPROT:Q7I246  
A;Accession: S71919  
A;Title: Proteolytic activation of grass carp (*Ctenopharyngodon idellus*) liver alcohol d  
A;Reference number: S71919  
A;Accession: S71919  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <TSU>  
A;Cross-references: UNIPROT:Q7I246  
A;Accession: PC2171  
triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (frag  
C;Species: Rhizopus niveus  
C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: PC2171  
R;Kondo, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.  
Biocci. Biotechnol. Biomed. 58, 1007-1012, 1994  
A;Title: Purification, characterization, and crystallization of two types of lipase fro  
A;Reference number: PC2171; MUID:94319055; PMID:7765029  
A;Accession: PC2171  
A;Molecule type: protein  
A;Residues: 1-10 <KOH>  
A;Cross-references: UNIPROT:Q7I166  
C;Comment: This enzyme catalyzes the hydrolysis of the ester bonds.  
C;Keywords: carboxylic ester hydrolase

Query Match 33.3%; Score 18; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPL 10  
Db 6 PPL 8

## RESULT 14

A61007 hementin (EC 3.4.-.-) - Amazon leech (fragment)  
 C;Species: Haementeria ghilianii (Amazon leech)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C;Accession: A61007  
 R;Swadsh, J. K.; Huang, I.Y.; Budzynski, A.Z.  
 J;Chromatogr. 502, 359-369, 1990  
 A;Title: Purification and characterization of hementin, a fibrinogenolytic protease from  
 A;Reference number: A61007; MUID:90256973; PMID:2187898  
 A;Accession: A61007  
 A;Molecule type: protein  
 A;Residues: 1-10 <SWA>  
 A;Cross-references: UNIPROT:Q7M3P9  
 C;Keywords: anticoagulant; hydrolase; saliva

Query Match 33.3%; Score 18; DB 2; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 5 DPTPPL 10  
 Db 5 EPEDPL 10

## RESULT 15

A61218 alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)  
 C;Species: Haynaldia villosa, Dactylyrum villosum

C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004

C;Accession: A61218  
 R;Shewry, P.R.; Sambelli, P.A.; Parmar, S.; Lafiandra, D.  
 Biochem. Genet. 29, 207-211, 1991  
 A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynald  
 A;Reference number: A61218; MUID:1313394; PMID:859356  
 A;Accession: A61218  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <SHE>  
 A;Cross-references: UNIPROT:Q7M1F7  
 C;Keywords: seed; storage protein

Query Match 31.5%; Score 17; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PTPL 10  
 Db 5 PVQL 9

search completed: January 6, 2005, 10:51:16  
 Job time : 40 SECS



DT 01-MAR-2004 (TREMBIREL. 26, Created)  
 DT 01-MAR-2004 (TREMBIREL. 26, Last annotation update)  
 DT 01-MAR-2004 (TREMBIREL. 26, Last annotation update)  
 DB Lectin (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterida;  
 OC lamiids; Solanales; Solanaceae; solanum.  
 NCBI\_TAXID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RA Miller D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,  
 RA Bolwell G.P.;  
 RT Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.  
 Characterization, immunolocalization and effects of wounding.";  
 RL Biochem. J. 283:813-821(1992).  
 DR PIR; S21288; S21288.  
 FT NON TER 8 8 8  
 SQ SEQUENCE 8 AA; 771 MW; C37775A771B5BDDA CRC64;

Query Match Score 24; DB 2; Length 8;  
 Best Local Similarity 44.4%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 RN QY 3 AMDPTPP 9  
 DB 2 ASTPSPP 8

RESULT 3  
 ID Q76MKS  
 AC Q76MKS  
 DT 05-JUL-2004 (TREMBIREL. 27, Created)  
 DT 05-JUL-2004 (TREMBIREL. 27, Last sequence update)  
 DR 05-JUL-2004 (TREMBIREL. 27, Last annotation update)  
 DB ATPas subunit 8 (Fragment).  
 GN Name=ATPas 8;  
 OG Eurypharynx pelecanoides (pelican eel).  
 OC Mitochondrion; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
 OC Eurypharyngidae; Eurypharynx.  
 NCBI\_TAXID=55117;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
 RA "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-  
 Scale Gene Rearrangements Originated Within the Eels.";  
 RA Mol. Biol. Evol. 20:1917-1924(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
 RA Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB046481; BAB87160.1; -.  
 KW Mitochondrion.  
 FT NON TER 10 10 10  
 SQ SEQUENCE 10 AA; 1217 MW; D99C5B75A76AA736 CRC64;

Query Match Score 23; DB 2; Length 10;  
 Best Local Similarity 42.6%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 RN QY 4 MDPTP 8  
 DB 4 LDPSp 8

RESULT 5  
 ID Q6SP94  
 AC Q6SP94  
 DT 05-JUL-2004 (TREMBIREL. 27, Created)  
 DT 05-JUL-2004 (TREMBIREL. 27, Last sequence update)  
 DR PF26 (Fragment).  
 RP Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 NCBI\_TAXID=3055;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CC-2290;  
 RX MEDLINE=2257034; PubMed=1684385;  
 RA Katiuk P., Lavigne M., Brazelton W.J., Haas N.A., Lefebvre P.A.,  
 RA Silflow C.D.;  
 RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome.";  
 RL Eukaryotic Cell 2:362-379(2003).  
 DR EMBL; AY54155; ARK2084.1; -.  
 FT NON TER 1 1 1  
 SQ SEQUENCE 9 AA; 1012 MW; DB0AB1B1B07776D CRC64;

Query Match Score 21; DB 2; Length 9;  
 Best Local Similarity 38.9%; Pred. No. 1.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 RN QY 6 PTAPP 9  
 DB 1 PAPP 4

RESULT 4  
 BAB87160

RESULT 6

ID	NAME=ure1;	PRT;	9 AA.
Q99193	PRELIMINARY;		
AC	Osmorganella morganii (Proteus morganii).	OS	
DT	01-NOV-1996 (TREMBrel. 01, Created)	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
DT	01-MAR-1996 (TREMBrel. 01, Last sequence update)	OC	Enterobacteriaceae; Morganella.
DT	01-MAR-2003 (TREMBrel. 23, Last annotation update)	OX	NCBI_TaxID=303;
DR	RpoB beta-subunit of RNA polymerase (Fragment).	RP	SEQUENCE.
DR	Pseudomonas putida.	RX	MEDLINE=90264298; PubMed=2345135;
DR	Bacterium; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	RA	Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.
DR	Pseudomonadaceae; Pseudomonas.	RT	"Morganella morganii urease"; purification, characterization, and
OX	[1]	RT	isolation of gene sequences."
RN	SEQUENCE FROM N.A.	RL	J. Bacteriol. 172:3073-3080 (1990).
RA	Borddin A.M., Danil'kovich A.V., Allikmets R.L., Rostovtsev V.M.,	CC	--I-- SUBUNIT: (Alpha, beta, gamma)(3) (BY similarity).
RA	Chemnov I.P., Azhikina T.I., Monastyrskaya S., Sverdlov D.,	CC	--I-- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).
RT	"Nucleotide sequence of the rpoB gene coding for the beta-subunit of	CC	--I-- SIMILARITY: Belongs to the urease gamma subunit family.
RT	RNA polymerase in Pseudomonas putida."	DR	PIR: C35389; C35389;
RL	DOK1. Biochem. 302:1251-1265 (1981).	DR	HAMAP; MP_00739; --I--
DR	EMBL; X15849; CAM3847.1; --I--	KW	Direct protein sequencing; Hydrolase.
PT	NON TER; 9 9	PT	NON TER; 10 10
SQ	SEQUENCE 9 AA; 852 MW; 5B416776DC76727 CRC64;	SQ	SEQUENCE 10 AA; 1171 MW; 4B313BCB07771A7 CRC64;
Query Match	38.9%; Score 21; DB 2; Length 9;	Query Match	38.9%; Score 21; DB 1; Length 10;
Best Local Similarity	75.0%; Pred. No. 1.8e+06;	Best Local Similarity	66.7%; Pred. No. 4.9e+03;
Matches	3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	6 PTTP 9	Qy	4 MDPTPP 9
Db	4 PAPP 7	Db	1 MQLTTPP 6
RESULT 7		RESULT 9	
AAR20844	PRELIMINARY;	P81898	PRELIMINARY;
AC	AAR20844;	ID	P81898
AC	14-APR-2004 (TREMBrel. 27, Created)	AC	P81898;
DT	14-APR-2004 (TREMBrel. 27, Last sequence update)	DT	01-MAR-2001 (TREMBrel. 16, Created)
DT	14-APR-2004 (TREMBrel. 27, Last annotation update)	DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)
DE	P276 (Fragment).	DT	01-JUN-2003 (TREMBrel. 24, Last annotation update)
OS	Chlamydomonas reinhardtii.	DB	Peptide-N-(N-acetyl)-beta-D-glucosaminyl)asparagine amidase A, small
OC	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;	DB	chain (Subunit B) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
OC	Chlamydomonadaceae; Chlamydomonas.	DR	glycosidase) (N-glycanase) (Fragment).
OX	NCBI_TaxID=3055;	OS	Prunus dulcis (Almond) (Prunus amygdalus).
RN	[1]	OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
RP	SEQUENCE FROM N.A.	OC	Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
RC	STRAIN=CC-2290;	OC	eurosid I; Rosales; Rosaceae; Amygdaloideae; Prunus.
RX	MEDLINE=22570934; PubMed=12684385;	OX	NCBI_TaxID=3755;
RA	Kathir P., LaVoie M., Brazelton W.J., Haas N.A., Lefebvre P.A.,	RN	[1]
RA	Siflow C.D.;	RP	SEQUENCE, AND CHARACTERIZATION.
RA	"Molecular map of the Chlamydomonas reinhardtii nuclear genome.";	RX	Published=9323720;
RA	Bukaryotic cell 2:362-379 (2003).	RA	Altmann P., Paschinger K., Dalik T., Vorauer K.'
RA	EMBL; AY454155; AAR20844.1; --	RT	"Characterisation of peptide-N4-(N-acetyl-beta-D-glucosaminyl)asparagine
FT	NON TER 1	RT	amidase A and its N-glycans";
SQ	SEQUENCE 9 AA; 1012 MW; DB0AAB1B1B07776D CRC64;	RL	Eur. J. Biochem. 252:118-123 (1998).
Query Match	38.9%; Score 21; DB 2; Length 9;	CC	-I- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
Best Local Similarity	75.0%; Pred. No. 1.8e+06;	CC	GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
Matches	3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	CC	GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
Qy	6 PTTP 9	CC	(SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
Db	1 PAPP 4	CC	CONTAINING AN ASPARTIC RESIDUE.
RESULT 8		CC	--I-- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN
URE3_MORMO	STANDARD;	CC	--I-- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELFP-
URE3_MORMO	PRT;	CC	DEGLYCOSYLATION.
AC	P173339;	CC	--I-- MASS SPECTROMETRY: MW=21247; METHOD=MAIDI.
DT	01-AUG-1990 (Rel. 15, Created)	DR	PIR; B59272; B59272.
DT	01-AUG-1990 (Rel. 15, last sequence update)	DR	F-hydrolase activity; IEA.
DT	05-JUL-2004 (Rel. 44, last annotation update)	GO	GO:0016787; GO:000224; F-peptide-N4-(N-acetyl-beta-D-glucosaminyl)aspa. . ; IEA.
DB	Urea gamma subunit (EC 3.5.1.5) (Urea amidohydrolase gamma subunit) (Urease 6 kDa subunit) (Fragment)	KW	Glycoprotein; Hydrolase.
DB	NON TER 10	SQ	SEQUENCE 10 AA; 1149 MW; 863278CA1E73771 CRC64;
Query Match	38.9%; Score 21; DB 2; Length 10;	Query Match	38.9%; Score 21; DB 2; Length 10;
Best Local Similarity	75.0%; Pred. No. 4.9e+03;	Best Local Similarity	75.0%; Pred. No. 4.9e+03;
Matches	3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Matches	3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	5 DPTP 8 ;    1 EPTP 4	Db	2 PIPP 5 
<b>RESULT 10</b>			
UFO4_MOUSE	STANDARD;	PRT;	7 AA.
ID UFO4_MOUSE			
AC P38642;			
DT 01-OCT-1994 (Rel. 30, Created)			
DT 01-OCT-1994 (Rel. 30, last sequence update)			
DT 05-JUL-2004 (Rel. 44, last annotation update)			
DB Unknown protein from 2D-PAGE of fibroblasts (P46) (Fragment).			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
KW NEBI_TaxID=10090;			
RN [1]			
RP Sequence.			
RC Tissue: Fibroblast;			
RX MEDLINE:95005907; PubMed=7523108;			
RA Merrick B.A., Patterson R.M., Wicher L.L., He C., Selkirk J.K.;			
RT Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.;			
RL Electrophoresis 15:735-745(1994).			
CC -- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown protein is: 5.0, its MW is: 46 kDa.			
KW direct protein sequencing.			
FT NON_TER 7 AA; 766 MW; 68640AB77762700 CRC64;			
SQ 7 AA; 766 MW; 68640AB77762700 CRC64;			
<b>Query Match 37.0%; Score 20; DB 1; Length 7; Best Local Similarity 75.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Db 1 PKPP 4</b>			
<b>RESULT 11</b>			
Q9IWZ3	PRELIMINARY;	PRT;	10 AA.
ID Q9IWZ3;			
AC 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)			
DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)			
DB lateinizing hormone/chorionic gonadotropin receptor homolog (Fragment).			
OS Rattus sp.			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphati; Muridae; Murinae; Rattus.			
OX NCBI_TaxId=10118;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE:Ovary;			
RX MEDLINE:96147985; PubMed=8571710;			
RA Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.;			
RT "Cloning and overexpression of rat ovary LH/hCG receptor cDNA in insect cells.";			
RL Acta Biol. Exp. Sinica 28:283-290(1995).			
DR S80660; AAB5701_1,-			
DR GO:0004872; Fireceptor activity; IEA.			
DR GO: GO:0005213; Fstructural constituent of chorion (sensu In. . . ; IEA.			
KW Chorion; Receptor.			
FT NON_TER 1 AA; 1129 MW; 09A5F22DC4177760 CRC64;			
SQ 1 AA; 1129 MW; 09A5F22DC4177760 CRC64;			
<b>Query Match 37.0%; Score 20; DB 2; Length 10; Best Local Similarity 75.0%; Pred. No. 7.3e+03; Indels 0; Gaps 0; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Db 6 PTTP 9</b>			
<b>RESULT 12</b>			
Q75595	PRELIMINARY;	PRT;	10 AA.
ID Q75595;			
AC Q75595;			
DT 01-NOV-1996 (TREMBLrel. 01, Created)			
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)			
DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)			
DB Tat protein (Fragment).			
GN Name=tat,			
OS Human immunodeficiency virus 1.			
OC Viruses; Retroviridae; Lentivirus;			
OX NCBI_TaxId=11676;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=93ETB8;			
RA Harris M.E., Mayan S., Kim B., Zeira M., Ferrari G., Brix D.L., McCutchan F.E.;			
RT "A cluster of HIV type 1 subtype C sequences from Ethiopia, observed in full genome analysis, is not sustained in subgenomic regions.", AIDS Res. Hum. Retroviruses 19:1125-1133(2003).			
RL Res. Hum. Retroviruses 19:1125-1133(2003).			
RN [2]			
RP SEQUENCE FROM N.A.			
RC STRAIN=93ETB8;			
RA Harris M.E., Birx D.L.;			
RT Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.			
RL [3]			
RP SEQUENCE FROM N.A.			
RC STRAIN=93ETB8;			
RA Kim B., McCutchan F.E.;			
RT Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.			
RL [4]			
RP SEQUENCE FROM N.A.			
RC STRAIN=93ETB8;			
RA Mayan S., Zeira M.;			
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.			
DR EMBL:AY255828; AAP76567_1; -			
SQ SEQUENCE 10 AA; 1154 MW; 22252E23276AB2D7 CRC64;			
Query Match 37.0%; Score 20; DB 2; Length 10;			

Best Local Similarity 50.0%; Pred. No. 7.3e+03; Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	4	MDP TPP 9	1	MSPVDP 6
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RESULT 14

ID	07M2M9	PRELIMINARY;	PRT;	9 AA.
AC	07M2M9;			
DT	01-MAR-2004	(TREMBLrel. 26, Created)		
DT	01-MAR-2004	(TREMBLrel. 25, Last sequence update)		
DE	Collagen alpha 2 (VI) chain (Fragment).			
OS	Bos taurus (Bovine)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovine; Bos;			
OC	NCBI_TAXID=9913;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE-83209648; PubMed-6852033; Jander R., Rautenberg J., Gianville R.W.;			
RT	"Further characterization of the three polypeptide chains of bovine and human short-chain collagen (intima collagen)."; Eur. J. Biochem. 133:39-46(1983).			
DR	PIR; S26508; S26508.			
FT	NON_TBR 1			
FT	NON_TBR 9			
SQ	SEQUENCE 9 AA; 876 MW; 68146776867605B CRC64;			

Query Match 35.2%; Score 19; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+04; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	5	DPTPPL 10	1	DRTPAL 6
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RESULT 15

FARS_MACRS	STANDARD;	PRT;	10 AA.
ID	F83278;		
AC	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DR	FMRFamide-like neuropeptide FLPS (DRTPALRF-amide).		
OS	Macrobrachium rosenbergii (Giant freshwater prawn).		
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Bivalacosta; Bucardiida; Decapoda; Pleocyemata; Caridea; Palaemonidae; Palaemonida; Macrobrachium;		
OC	OK		
RN	NCBI_TAXID=19674;		
RP	SEQUENCE, AND MASS SPECTROMETRY.		
RC	TISSUE-Eyesstalk;		
RA	Sithigornkul P., Saraiethongkum W., Jaideechoey S., Longyant S.,		
RT	"Novel FMRFamide-like neuropeptides from the eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";		
RL	Comp. Biochem. Physiol. 120B:587-595(1998).		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- MASS SPECTROMETRY: MW=1243.4; METHOD=MALDI; RANGE=1-10; NOTE=Ref.1.		
CC	-1- SIMILARITY: Belongs to the FMR (FMRFamide related peptide) family.		
CC	GO: GO:007118; P:neuropeptide signaling pathway; TAS.		
DR	Amidation; Direct protein Sequencing; Neuropeptide.		
KW	Mod RES 10 10 Phenylalanine amide.		
FT	SEQUENCE 10 AA; 1244 MW; 9A1A533:072DC71 CRC64;		

Query Match 35.2%; Score 19; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+04; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	5	DPTPPL 10	1	DRTPAL 6
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Search completed: January 6, 2005, 10:50:32  
Job time : 189 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: January 6, 2005, 10:23:57 ; search time 149 seconds  
 (without alignments)  
 24.076 Million cell updates/sec

Title: US-10-047-945-1  
 Perfect score: 54  
 Sequence: 1 LKAMNDPTPPL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5  
 Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:

444336

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%  
 Listing first 45 summaries

Database :

- 1: A\_Geneseq\_23Seq04;\*
- 2: geneseqD19808;\*
- 3: geneseqD20008;\*
- 4: geneseqD20018;\*
- 5: geneseqD20028;\*
- 6: geneseqD2013as;\*
- 7: geneseqD2003bs;\*
- 8: geneseqD2004as;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

\* Maximum DB seq length: 0

Maximum Match 100%  
 Listing first 45 summaries

Post-processing: Minimum Match 0%

Maximum Match 100%  
 Listing first 45 summaries

Database :

A\_Geneseq\_23Seq04;\*

geneseqD19808;\*

geneseqD20008;\*

geneseqD20018;\*

geneseqD20028;\*

geneseqD2013as;\*

geneseqD2003bs;\*

geneseqD2004as;\*

geneseqD2005as;\*

geneseqD2006as;\*

geneseqD2007as;\*

geneseqD2008as;\*

geneseqD2009as;\*

geneseqD2010as;\*

geneseqD2011as;\*

geneseqD2012as;\*

geneseqD2013as;\*

geneseqD2014as;\*

- 1: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
 Adk1547 Peptide f  
 Adr1547 YES prote  
 Adr93336 YES prote  
 Aay48003 Immuno  
 Ade97778 Immuno  
 Aar56874 Cystatice  
 Aar63465 Trypsin M  
 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito

- 2: AAW53843 standard; peptide; 10 AA.  
 AC  
 AAW53843;  
 XX  
 DT 08-JUL-1998 (first entry)  
 XX  
 DB N-terminus of opossum LTNF.  
 KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;  
 KW anti-hemorrhagic protein; Blapidae; Viperidae; sea snake; snake bite;  
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;  
 KW histamine reaction treatment.
- 3: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
 Adr1547 Peptide f  
 Adr93336 YES prote  
 Aay48003 Immuno  
 Ade97778 Immuno  
 Aar56874 Cystatice  
 Aar63465 Trypsin M  
 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
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 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 4: AAW53843 N-terminal Abw53843 Synthetic  
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 Abb80227 Synthetic  
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 Abb78478 Gum arab  
 Asy47988 Immuno  
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 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 5: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
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 Adr1547 Peptide f  
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 Adc5474 Trypsin m  
 Add10251 Mosquito
- 6: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
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 Aar56874 Cystatice  
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 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 7: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
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 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito

Maximum DB seq length: 0

Maximum Match 100%  
 Listing first 45 summaries

Post-processing: Minimum Match 0%

Maximum Match 100%  
 Listing first 45 summaries

Database :

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geneseqD19808;\*

geneseqD20008;\*

geneseqD20018;\*

geneseqD20028;\*

geneseqD2013as;\*

geneseqD2003bs;\*

geneseqD2004as;\*

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geneseqD2006as;\*

geneseqD2007as;\*

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geneseqD2011as;\*

geneseqD2012as;\*

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geneseqD2031as;\*

geneseqD2032as;\*

geneseqD2033as;\*

geneseqD2034as;\*

geneseqD2035as;\*

geneseqD2036as;\*

geneseqD2037as;\*

geneseqD2038as;\*

geneseqD2039as;\*

geneseqD2040as;\*

- 1: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
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 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 2: AAW53843 standard; peptide; 10 AA.  
 AC  
 AAW53843;  
 XX  
 DT 08-JUL-1998 (first entry)  
 XX  
 DB N-terminus of opossum LTNF.  
 KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;  
 KW anti-hemorrhagic protein; Blapidae; Viperidae; sea snake; snake bite;  
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;  
 KW histamine reaction treatment.
- 3: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
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 Aaw19715 Digestion  
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 Ab37945 Trypsin m  
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- 4: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
 Adr1547 Peptide f  
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 Aar63465 Trypsin M  
 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
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 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 5: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
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 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
 Adr1547 Peptide f  
 Adr93336 YES prote  
 Aay48003 Immuno  
 Ade97778 Immuno  
 Aar56874 Cystatice  
 Aar63465 Trypsin M  
 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 6: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
 Adr1547 Peptide f  
 Adr93336 YES prote  
 Aay48003 Immuno  
 Ade97778 Immuno  
 Aar56874 Cystatice  
 Aar63465 Trypsin M  
 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 7: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
 Adr1547 Peptide f  
 Adr93336 YES prote  
 Aay48003 Immuno  
 Ade97778 Immuno  
 Aar56874 Cystatice  
 Aar63465 Trypsin M  
 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito

Maximum DB seq length: 0

Maximum Match 100%  
 Listing first 45 summaries

Post-processing: Minimum Match 0%

Maximum Match 100%  
 Listing first 45 summaries

Database :

A\_Geneseq\_23Seq04;\*

geneseqD19808;\*

geneseqD20008;\*

geneseqD20018;\*

geneseqD20028;\*

geneseqD2013as;\*

geneseqD2003bs;\*

geneseqD2004as;\*

geneseqD2005as;\*

geneseqD2006as;\*

geneseqD2007as;\*

geneseqD2008as;\*

geneseqD2009as;\*

geneseqD2010as;\*

geneseqD2011as;\*

geneseqD2012as;\*

geneseqD2013as;\*

geneseqD2014as;\*

geneseqD2015as;\*

geneseqD2016as;\*

geneseqD2017as;\*

geneseqD2018as;\*

geneseqD2019as;\*

geneseqD2020as;\*

geneseqD2021as;\*

geneseqD2022as;\*

geneseqD2023as;\*

geneseqD2024as;\*

geneseqD2025as;\*

geneseqD2026as;\*

geneseqD2027as;\*

geneseqD2028as;\*

geneseqD2029as;\*

geneseqD2030as;\*

geneseqD2031as;\*

geneseqD2032as;\*

geneseqD2033as;\*

geneseqD2034as;\*

geneseqD2035as;\*

geneseqD2036as;\*

geneseqD2037as;\*

geneseqD2038as;\*

- 1: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
 Adr1547 Peptide f  
 Adr93336 YES prote  
 Aay48003 Immuno  
 Ade97778 Immuno  
 Aar56874 Cystatice  
 Aar63465 Trypsin M  
 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 2: AAW53843 standard; peptide; 10 AA.  
 AC  
 AAW53843;  
 XX  
 DT 08-JUL-1998 (first entry)  
 XX  
 DB N-terminus of opossum LTNF.  
 KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;  
 KW anti-hemorrhagic protein; Blapidae; Viperidae; sea snake; snake bite;  
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;  
 KW histamine reaction treatment.
- 3: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
 Adr1547 Peptide f  
 Adr93336 YES prote  
 Aay48003 Immuno  
 Ade97778 Immuno  
 Aar56874 Cystatice  
 Aar63465 Trypsin M  
 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 4: AAW53843 N-terminal Abw53843 Synthetic  
 Abb80222 Synthetic  
 Abb80227 Synthetic  
 Abb80228 Synthetic  
 Abb8473 Mutated p  
 Abb78481 Gum arabi  
 Abb78478 Gum arab  
 Asy47988 Immuno  
 Asy86825 Telomeras  
 Asy86735 Telomeras  
 Adk07609 Hepatitis  
 Adr1547 Peptide f  
 Adr93336 YES prote  
 Aay48003 Immuno  
 Ade97778 Immuno  
 Aar56874 Cystatice  
 Aar63465 Trypsin M  
 Aar80074 P2 analog  
 Aaw19715 Digestion  
 Aew69749 Digestion  
 Ab37945 Trypsin m  
 Ab3061 Trypsin m  
 Adp58325 Trypsin m  
 Adc5474 Trypsin m  
 Add10251 Mosquito
- 5: AAW53843 N-terminal Abw53



Query Match 92.6%; Score 50; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LKAMDPTPP 9
Db	1 LKAMDPTPP 9

RESULT 4  
 ID ABB80228 standard; peptide; 8 AA.  
 XX  
 AC ABB80228;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DB Synthetic LTNF, LT-8.  
 XX  
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLB; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200306471-A2.  
 XX  
 PD 24-JUL-2003.  
 XX  
 PP 14-JAN-2003; 2003WO-US001044.  
 XX  
 PR 14-JAN-2002; 2002US-00047945.  
 XX  
 PA (LTNP/ ) LIPPS B V.  
 PA (LTNP/ ) LIPPS P W.  
 XX  
 PT LIPPS BV, LIPPS PW;  
 XX  
 DR WPI; 2003-636703/60.

XX  
 PT Assaying a human endogenous protein (e.g. IgB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.  
 PT  
 XX  
 PS Claim 7, Page 4; 24pp; English.

XX  
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgB levels, e.g. asthma, diabetes, Addison's disease or Hodgkin's disease. In particular, the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA

XX  
 Sequence 8 AA;

Query Match 79.6%; Score 43; DB 7; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 LKAMDPTPP 8
Db	1 LKAMDPTPP 8

RESULT 5  
 ID ABB68473 standard; peptide; 6 AA.  
 XX  
 AC ABB68473;  
 XX  
 DT 23-JUL-2001 (first entry)  
 XX  
 DB Mutated peptide derived from integrase of Ty5-6p, residues 1092-1097.  
 XX  
 KW Retrotransposon; polproteins; integrase; Ty1-copia; silent chromatin; chromosomal integration; chromosomal targeting; Ty5; aging; oncogene.  
 XX  
 PN US622647-B1.  
 XX  
 PD 08-MAY-2001.  
 XX  
 PF 15-JAN-1999; 99US-00232446.  
 XX  
 PR 15-JAN-1998; 98US-0071333P.  
 XX  
 PA (IOWA ) UNIV IOWA STATE RES FOUND INC.  
 XX  
 PT Voytas DF, Gai X;  
 XX  
 DR WPI; 2001-342676/36.  
 XX  
 PS Targeting integration of retrotransposon or retrovirus into silent chromatin by transforming a cell with modified integrase having a coding sequence for a peptide portion that interacts with chromatin at desired sites.  
 XX  
 CC Claim 13; Col 56; 41pp; English.  
 CC The present sequence represents a mutated portion of an integrase. The specification describes a method for targeting integration of retrotransposon of Ty1-copia group to desired location on a chromosome. The method uses a modified integrase in a retrotransposon which modified integrase contains a coding sequence for a peptide portion which specifically binds to protein bound to the chromosome or to particular nucleic acid sequences on chromosome. The method is useful for targeting integration of a retrotransposon of the Ty1-copia group to a desired location on a chromosome, especially into silent chromatin. The silent chromatin targeting of Ty5 is useful for tagging genes which are affected by aging and for studying oncogenes  
 XX  
 Sequence 6 AA;

Query Match 55.6%; Score 30; DB 4; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	4 MDPTPP 9
Db	1 LDPSPP 6

RESULT 6  
 ID ABB78481 standard; peptide; 8 AA.  
 XX  
 AC ABB78481;  
 XX  
 DT 09-JUL-2002 (first entry)

XX  
DE Gum arabic glycoprotein (GAGE) peptide motif SEQ ID NO:168.  
XX plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;  
KW HRGp; repetitive proline-rich protein; RPRP; arabinogalactan protein;  
KW AGP; plant gum.  
XX OS Synthetic.  
XX Acacia senegal.  
PN WO200178503-A2.  
XX PD 25-OCT-2001.  
XX PS Claim 5; Page 121; 326pp; English.  
XX PR 12-APR-2001; 2001WO-US012336.  
XX PT 12-APR-2000; 2000US-00547693.  
XX DR (UWORH-) UNIV OHIO.  
XX PA Kieliszewski MJ;  
XX PI WPI; 2002-041307/05.  
XX PT Nucleic acids and proteins useful for producing hydroxy-proline rich  
XX PT glycoproteins in plants.  
XX PS Claim 5; Page 121; 326pp; English.  
XX CC The present invention describes synthetic genes encoding plant gums and  
CC other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic  
CC acids that encode them. The nucleic acids, proteins and methods from the  
CC present invention may be used to produce HRGPs, repetitive proline-rich  
CC proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via  
CC recombinant methodologies. Also described is the expression of synthetic  
CC genes designed from repetitive peptide sequences, such as glycoproteins  
CC (including the peptide sequences of gum arabic glycoprotein (GAGE)).  
CC ABLS1730 to ABLS189 and ABB78401 to ABB7854 represent sequences used in  
CC the exemplification of the present invention  
XX CC Sequence 8 AA;  
XX SQ Query Match 55.6%; Score 30; DB 5; Length 8;  
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX Qy 6 PTTPPL 10  
XX Db 3 PTTPPL 7  
XX AC AAY47988 standard; peptide; 9 AA.  
XX DT 01-DEC-1999 (first entry)  
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #2599.  
XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
KW immune response; T cell activation; major histocompatibility complex;  
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
KW vaccine; immunisation.  
XX OS Synthetic.  
XX OS Homo sapiens.  
AC WO9945954-A1.  
XX PN 09-JUL-2002 (first entry)  
XX DT 16-SEP-1999.  
DB Gum arabic glycoprotein (GAGE) peptide motif SEQ ID NO:165.  
XX Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;  
KW HRGp; repetitive proline-rich protein; RPRP; arabinogalactan protein;  
KW AGP; plant gum.  
OS Acacia senegal.  
OS Synthetic.  
XX PN WO200178503-A2.  
XX PD 25-OCT-2001.  
XX PP 12-APR-2001; 2001WO-US012336.  
XX PR 12-APR-2000; 2000US-00547693.  
XX PA (UWORH-) UNIV OHIO.  
XX PI Kieliszewski MJ;  
XX DR WPI; 2002-041307/05.  
XX PT Nucleic acids and proteins useful for producing hydroxy-proline rich  
XX PT glycoproteins in plants.  
XX PS Claim 5; Page 121; 326pp; English.  
XX CC The present invention describes synthetic genes encoding plant gums and  
CC other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic  
CC acids that encode them. The nucleic acids, proteins and methods from the  
CC present invention may be used to produce HRGPs, repetitive proline-rich  
CC proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via  
CC recombinant methodologies. Also described is the expression of synthetic  
CC genes designed from repetitive peptide sequences, such as glycoproteins  
CC (including the peptide sequences of gum arabic glycoprotein (GAGE)).  
CC ABLS1730 to ABLS189 and ABB78401 to ABB7854 represent sequences used in  
CC the exemplification of the present invention  
XX SQ Sequence 10 AA;  
XX Query Match 55.6%; Score 30; DB 5; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX Qy 6 PTTPPL 10  
XX Db 3 PTTPPL 7  
XX AC AAY47988;  
XX DT 01-DEC-1999 (first entry)  
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #2599.  
XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
KW immune response; T cell activation; major histocompatibility complex;  
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
KW vaccine; immunisation.  
XX OS Synthetic.  
XX OS Homo sapiens.  
AC WO9945954-A1.  
XX PN 13-MAR-1998; 98WO-US005039.  
XX PR 13-MAR-1998; 98WO-US005039.  
XX PA (EPIIM-) EPIIMMUNE INC.  
XX Sette A, Kubo RT, Sidney J, Celis B, Grey HM, Southwood S;  
XX PI DR WPI; 1999-551214/45.  
XX PT New immunogenic peptides with HLA binding motif, useful in treatment and  
XX PT diagnosis of cancers and viral diseases.  
XX PS Claim 1; Page 131; 150pp; English.

XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leucocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A2.1, or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above

SQ Sequence 9 AA;

Query Match 51.9%; Score 28; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPPL 10  
Db 1 DPTPPL 6

RESULT 9

AAY86825

AAY86825 standard; peptide; 9 AA.

AC AAY86825;

DT 05-MAY-2000 (first entry)

DB Telomerase peptide #240.

XX Telomerase; antigenic peptide; cancer; therapy; human; tumour cell; malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma; telomerase T lymphocyte.

OS Homo sapiens.

XX WO200002581-A1.

XX PD 20-JAN-2000.

PP 30-JUN-1999; 99WO-N0000220.

PR 08-JUL-1998; 98NO-00003141.

PA (NIRD ) NORSK HYDRO AS.

XX PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

PI Saaboe-Larsen S;

XX DR WPI; 2000-145727/13.

PT Protein or peptide fragments useful in the treatment and prophylaxis of

XX cancer in mammals.

PS Claim 12; Page 35; 53pp; English.

XX This sequence represents a telomerase peptide of the invention, and can

CC be used in a method for the treatment or prophylaxis of cancer. The

CC sequences are useful in the treatment or prophylaxis of cancer

CC especially, breast, lung, ovarian, cervical, colorectal, prostate or

CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary

CC tract carcinomas. They are useful for generating telomerase T lymphocytes

CC capable of recognising and destroying tumour cells in a mammal,

CC comprising culturing T lymphocytes obtained from the mammal with the

CC peptides. Telomerase protein is expressed only by tumour cells, hence, T

CC other body cells are not targeted or destroyed by telomerase specific T

CC cells. Note: This sequence was indexed from WO200002581, which is the

CC first major country equivalent to N09803141

SQ Sequence 9 AA;

Query Match 51.9%; Score 28; DB 3; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDPTPPL 10  
Db 1 RADPDPPEL 9

RESULT 10

AAY86735

AAY86735 standard; peptide; 9 AA.

AC AAY86735;

DT 05-MAY-2000 (first entry)

DB Telomerase peptide #150.

XX KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell; malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma; telomerase T lymphocyte.

XX OS Homo sapiens.

XX PN WO200002581-A1.

XX PD 20-JAN-2000.

PP 30-JUN-1999; 99WO-N0000220.

PR 08-JUL-1998; 98NO-00003141.

PA (NIRD ) NORSK HYDRO AS.

XX PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

PI Saaboe-Larsen S;

XX DR WPI; 2000-145727/13.

PT Protein or peptide fragments useful in the treatment and prophylaxis of

XX cancer in mammals.

PS Claim 12; Page 35; 53pp; English.

XX This sequence represents a telomerase peptide of the invention, and can

CC be used in a method for the treatment or prophylaxis of cancer. The

CC sequences are useful in the treatment or prophylaxis of cancer

CC especially, breast, lung, ovarian, cervical, colorectal, prostate or

CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary

CC tract carcinomas. They are useful for generating telomerase T lymphocytes

CC capable of recognising and destroying tumour cells in a mammal,

CC comprising culturing T lymphocytes obtained from the mammal with the

CC peptides. Telomerase protein is expressed only by tumour cells, hence, T

CC other body cells are not targeted or destroyed by telomerase specific T

CC cells. Note: This sequence was indexed from WO200002581, which is the

CC first major country equivalent to N09803141

SQ Sequence 9 AA;

Query Match 51.9%; Score 28; DB 3; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.7e+06;

CC This sequence represents a telomerase peptide of the invention, and can

CC be used in a method for the treatment or prophylaxis of cancer. The

CC sequences are useful in the treatment or prophylaxis of cancer

CC especially, breast, lung, ovarian, cervical, colorectal, prostate or

CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary

CC tract carcinomas. They are useful for generating telomerase T lymphocytes

Matches	5;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;	DT
Qy	2	KAMPTPPL	10							XX
Db	1	RAQDPPPEL	9							XX
RESULT 11										
ADK07609										KW
ID	ADK07609	standard;	peptide;	9 AA.						antigen; epitope; immunogenic target protein; PSA; HBV <sub>C</sub> ; HBV <sub>B</sub> ; EBV; HIV <sub>I</sub> ; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human Papilloma virus; P51; c-EBRB2; MAGB-1; melanoma antigen-1; core antigen; Surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen.
AC	ADK07609;									XX
XX										OS
DT	06-MAY-2004	(first entry)								XX
XX										PN
DB	Hepatitis C virus	CTU epitope peptide #5439.								XX
XX	KW	pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; epitope peptide; HLA-allele; CTU.								XX
OS	Hepatitis C virus.									XX
XX	PN	W02004011650-A2.								XX
XX	XX									XX
PD	05-FEB-2004.									XX
XX	XX									XX
PF	24-JUL-2003;	2003WO-EP008112.								XX
PR	24-JUL-2002;	2002AT-00001124.								XX
PR	11-JUL-2003;	2003EP-00450171.								XX
PA	(INVE-) INTERCELL AG.									XX
XX	PT	Mattner P, Schmidt W, Habel A;								XX
XX	DR	WPI; 2004-169243/16.								XX
XX	PT	New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.								XX
XX	PT	Claim 14; Page 162; 220pp; English.								XX
CC	This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a hepatitis C virus CTU epitope peptide of the invention.								XX	
CC	Sequence 9 AA;									XX
SQ										XX
RESULT 12										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
RESULT 13										
AAR93336	Query Match	51.9%; Score 28; DB 2; Length 10;								
ID	Best Local Similarity	83.3%; Pred. No. 5.4e+02;								
Matches	5;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;	
Qy	5	DPTPPL	10							XX
Db	5	DPTPPM	10							XX
SYNTHETIC	Sequence 10 AA;									XX
RESULT 14										
AAR93336	Query Match	51.9%; Score 28; DB 2; Length 10;								
ID	Best Local Similarity	83.3%; Pred. No. 5.4e+02;								
Matches	5;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;	
Qy	5	DPTPPL	10							XX
Db	5	DPTPPM	10							XX
SYNTHETIC	Sequence 10 AA;									XX
RESULT 15										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 16										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 17										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 18										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 19										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 20										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 21										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 22										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 23										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 24										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 25										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 26										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 27										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 28										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 29										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 30										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							XX
Db	4	PTPPM	8							XX
SYNTHETIC	Sequence 9 AA;									XX
RESULT 31										
AAR61547	Query Match	51.9%; Score 28; DB 8; Length 9;								
ID	Best Local Similarity	80.0%; Pred. No. 1.7e-06;								
Matches	4;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	6	PTPPL	10							

PN WO9524419-A1.  
 XX PF 13-MAR-1998; 98WO-US005039.  
 PD XX 14-SEP-1995.  
 XX PR 13-MAR-1995; 95WO-US003208.  
 XX PR 11-MAR-1994; 94US-00209835.  
 XX DR 06-JAN-1995; 95US-00369832.  
 PA XX (ARIA-) ARIAD PHARM INC.  
 XX PT RICKLES RJ, Brugge JS, Botfield MC, Zoller MD;  
 XX DR WPI; 1995-328231/42.  
 PS XX Identification of peptide(s) binding specifically to SH3 domains - for  
 PT use in inhibiting interactions mediated by SH3 domains in treatment of  
 PT e.g. osteoporosis and cancer.  
 XX Disclosure: Fig 1; 74pp; English.  
 CC The sequences given in AAR32272-342 represent peptides which are SH3  
 CC ligands/SH3 binding agents. They represent a biased phage library which  
 CC comprises six random amino acids flanking the tetrapeptide -PPIP which  
 CC was identified as a recognition sequence for the src SH3 domain. These  
 CC sequences were identified using the method of the invention. The method  
 CC comprises contacting the SH3 domain with a mixture of peptides under  
 CC conditions permitting a ligand to bind to an SH3 domain to form a  
 CC complex. Any unbound peptides are removed and the complexed peptide  
 CC ligands are dissociated from the complexes. The selected peptides are  
 CC enriched by re-contacting them with the SH3 domain and then candidates  
 CC which bind to the SH3 domain are detected. The isolated SH3 binding  
 CC peptides may be used in the diagnosis, prevention and treatment of  
 CC conditions or diseases resulting from cellular processes mediated by an  
 CC SH3-based interaction. Such diseases include Paget's disease. Other  
 CC conditions treatable with these peptides include retinosis, rheumatoid  
 CC arthritis, gout and other problems in which an SH3 of neutrophil oxidase  
 CC p47 and p67 complex is implicated, etc  
 XX Sequence 10 AA:  
 Query Match 51.9%; Score 28; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY OY 2 KAMDPPTPL 10  
 Db 1 KAKRPLPPI 9  
 RESULT 14  
 AAY48003 standard; peptide; 10 AA.  
 AC XX  
 AC XX  
 AC AAY48003; DT 01-DEC-1999 (first entry)  
 XX Immunogenic peptide having a human leukocyte antigen binding motif #2614.  
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX WO994554-A1.  
 PN XX 16-SEP-1999.

---

PS XX New immunogenic peptides with HLA binding motif, useful in treatment and  
 PT diagnosis of cancers and viral diseases.  
 XX Claim 1; Page 132; 150pp; English.  
 CC AAY45390 to AAY8214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also known  
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides  
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2  
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against  
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes  
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an  
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather  
 CC than the intact foreign antigen itself, and are particularly important in  
 CC tumour rejection and in fighting viral infections. The peptides are  
 CC therefore useful therapeutically to treat or prevent viral infections and  
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B  
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to  
 CC elicit an immune response in individuals susceptible or otherwise at risk  
 CC of viral infection or cancer, or used to treat chronic or acute  
 CC conditions. They are also useful diagnostically, and can be used to  
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with  
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a  
 CC patient. The polynucleotides encoding the immunogenic peptides are also  
 CC useful therapeutically and for immunisation as above  
 XX Sequence 10 AA;  
 Query Match 51.9%; Score 28; DB 2; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY OY 5 DPTPPL 10  
 Db 1 DPPTPL 6  
 RESULT 15  
 ADE97778 standard; peptide; 10 AA.  
 AC XX  
 AC XX  
 AC ADE97778; DT 12-FEB-2004 (first entry)  
 XX Immunogenic HLA-A2.1 binding peptide #260.  
 KW Cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;  
 KW nephrotoxic; neuroprotective; antirheumatic; thyromimetic;  
 KW immunopressive; dermatological; muscular; nephrotoxic; thymomimetic;  
 KW haemostatic; antithyroid; antiaemic; anabolic; hyperensive;  
 KW immunogenic peptide composition; immune response; prostate cancer;  
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;  
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;  
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;  
 KW Sjogren syndrome; sclerodema; polyvostitis; dermatomyositis;  
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;  
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;  
 KW pemphigus; glomerulonephritis; Goodpasture's syndrome;  
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;  
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;  
 KW human leukocyte antigen A2.1; HLA A2.1;  
 KW immunogenic HLA-A2.1-binding peptide.

XX  
 OS Synthetic.  
 XX  
 PN US2003185822-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PP 03-APR-2002; 2002US-00116557.  
 XX  
 PR 05-MAR-1993; 93US-0027145.  
 PR 04-JUN-1993; 93US-00073205.  
 PR 29-NOV-1993; 93US-00159184.  
 PR 02-DEC-1994; 94US-00349177.  
 XX  
 PA (GREY/) GREY H M.  
 PA (SETTE/) SETTE A.  
 PA (SIDN/) SIDNEY J.  
 XX  
 PT Grey HM, Sette A, Sidney J,  
 DR XX  
 WPI; 2004-041186/04.  
 XX  
 PT Immunogenic peptide composition for preventing, treating or diagnosing  
 pathological states, e.g. prostate cancer, hepatitis B and C, Acquired  
 PT immunodeficiency Syndrome, and renal carcinoma, includes conserved  
 PT residues at specified positions.  
 XX  
 PS Example 11; Page 25; 38pp; English.  
 CC  
 CC The invention describes an immunogenic peptide composition comprising 9  
 CC residues including a first conserved residue at a second position from N-  
 CC terminus, and a second conserved residue at C-terminal position. The  
 CC inventive peptide composition is used to elicit an immune response  
 CC against a desired antigen for preventing, treating or diagnosing  
 pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,  
 AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus  
 CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune  
 CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,  
 CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic  
 CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing  
 CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,  
 CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,  
 CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic  
 CC purpura, Grave's disease, and Addison's disease. The invention defines  
 CC positions within a motif enabling the selection of the peptides which  
 CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the  
 CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 51.9%; Score 28; DB 8; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	5	DPTPPL 10
Db	5	DPTPPL 10

Search completed: January 6, 2005, 10:47:18  
 Job time : 151 sec

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Om protein - protein search, using SW model

Run on: January 6, 2005, 10:50:39 ; Search time 141 seconds  
                   (without alignments) ; 25.572 Million cell updates/sec

Title: US-10-047-945-1  
 Perfect score: 54  
 Sequence: 1 LKAMDPPTPL 10

Scoring table: BIOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 183704

Minimum DB seq length: 0  
 Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications\_ARI,\*

1: /cgmn\_6/ptodata/1/pubpaa/us07\_PUBCOMB.pep:\*

2: /cgmn\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgmn\_6/ptodata/1/pubpaa/us06\_NET\_PUB.pep:\*

4: /cgmn\_6/ptodata/1/pubpaa/us06\_PUBCOMB.pep:\*

5: /cgmn\_6/ptodata/1/pubpaa/us07\_NEW\_PUB.pep:\*

6: /cgmn\_6/ptodata/1/pubpaa/PCUTS\_PUBCOMB.pep:\*

7: /cgmn\_6/ptodata/1/pubpaa/us08\_NEW\_PUB.pep:\*

8: /cgmn\_6/ptodata/1/pubpaa/us08\_PUBCOMB.pep:\*

9: /cgmn\_6/ptodata/1/pubpaa/us09\_PUBCOMB.pep:\*

10: /cgmn\_6/ptodata/1/pubpaa/us09C\_PUBCOMB.pep:\*

11: /cgmn\_6/ptodata/1/pubpaa/us09\_NEW\_PUB.pep:\*

12: /cgmn\_6/ptodata/1/pubpaa/us09A\_PUBCOMB.pep:\*

13: /cgmn\_6/ptodata/1/pubpaa/us10A\_PUBCOMB.pep:\*

14: /cgmn\_6/ptodata/1/pubpaa/us10B\_PUBCOMB.pep:\*

15: /cgmn\_6/ptodata/1/pubpaa/us10C\_PUBCOMB.pep:\*

16: /cgmn\_6/ptodata/1/pubpaa/us10D\_PUBCOMB.pep:\*

17: /cgmn\_6/ptodata/1/pubpaa/us11\_NEW\_PUB.pep:\*

18: /cgmn\_6/ptodata/1/pubpaa/us11\_NEW\_PUB.pep:\*

19: /cgmn\_6/ptodata/1/pubpaa/us60\_NEW\_PUB.pep:\*

20: /cgmn\_6/ptodata/1/pubpaa/us60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match Length	DB ID	Description
1	54	100.0	10	14	US-10-047-945-1
2	50	92.6	9	14	US-10-047-945-6
3	43	79.6	8	14	US-10-047-945-7
4	30	55.6	8	15	US-10-437-708-168
5	30	55.6	8	17	US-10-257-199-168
6	30	55.6	10	15	US-10-437-708-165
7	30	55.6	10	17	US-10-257-199-165
8	28	51.9	9	US-08-344-824-273	
9	28	51.9	10	US-08-344-824-381	
10	27	50.0	8	US-09-758-128-20	
11	27	50.0	8	US-09-758-128-23	
12	27	50.0	8	US-09-758-128-25	
13	27	50.0	8	US-09-758-128-29	

RESULT 1

; US-10-047-945-1  
 ; Sequence 1, Application US/10047945  
 ; Publication No. US20030157555A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LIPPS, FREDERICK W.  
 ; APPLICANT: LIPPS, BINIE V.  
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
 ; TITLE OF INVENTION: (198) IMPLICATED DISORDERS  
 ; FILE REFERENCE: FWIPIATO15US  
 ; CURRENT APPLICATION NUMBER: US/10/047-945  
 ; CURRENT FILING DATE: 2002-01-14  
 ; PRIORITY FILING DATE:  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS  
 ; SEQ ID NO 1  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY:  
 ; LOCATION:  
 ; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM  
 ; OTHER INFORMATION: US 5,576,297.  
 ; OTHER INFORMATION: US-10-047-945-1

Qy 1 LKAMDPPTPL 10  
 Db 1 LKAMDPPTPL 10

RESULT 2  
US-10-047-945-6  
; Sequence 6 Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (198) IMPLICATED DISORDERS  
; FILE REFERENCE: FWFAT0105US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIORITY APPLICATION NUMBER:  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; FEATURE:  
; LOCATION: OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; FEATURE:  
; LOCATION: OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; NAME/KEY: SITE  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; NAME/KEY: SITE  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Unknown  
; NAME/KEY:  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; NAME/KEY: SITE  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Unknown  
; NAME/KEY:  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; FEATURE:  
; LOCATION: OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; FEATURE:  
; LOCATION: OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; NAME/KEY: SITE  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; FEATURE:  
; LOCATION: OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; FEATURE:  
; LOCATION: OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; NAME/KEY: SITE  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

RESULT 4  
US-10-437-708-168  
; Sequence 168 Application US/10437708  
; Publication No. US2004009555A1  
; GENERAL INFORMATION:  
; APPLICANT: Kieliszewski, Marcia  
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
; TITLE OF INVENTION: Glycoproteins  
; FILE REFERENCE: OHT-04089  
; CURRENT APPLICATION NUMBER: US/10/437,708  
; CURRENT FILING DATE: 2003-05-14  
; PRIORITY APPLICATION NUMBER: US/09/547,693  
; PRIORITY FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 236  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 168  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial/Unknown  
; NAME/KEY:  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; NAME/KEY: SITE  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.  
; SEQ ID NO 168  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial/Unknown  
; NAME/KEY:  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; NAME/KEY: SITE  
; FEATURE:  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

QY 6 PRPPL 10 ; ; ; ; ;  
Db 1 PRPPL 5 ; ; ; ; ;

RESULT 6 ; ; ; ; ;  
US-10-437-708-165 ; ; ; ; ;  
; Sequence 165, Application US/10437708  
; Publication No. US2004009555A1 ; ; ; ; ;  
; GENERAL INFORMATION ; ; ; ; ;  
; APPLICANT: Kielisiewski, Marcia ; ; ; ; ;  
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
; FILE REFERENCE: ONU-04089 ; ; ; ; ;  
; CURRENT APPLICATION NUMBER: US/10/437,708 ; ; ; ; ;  
; PRIORITY FILING DATE: 2003-05-14 ; ; ; ; ;  
; NUMBER OF SEQ ID NOS: 236 ; ; ; ; ;  
; SOFTWARE: PatentIn version 3.0 ; ; ; ; ;  
; SEQ ID NO 165 ; ; ; ; ;  
; LENGTH: 10 ; ; ; ; ;  
; TYPE: PRPPL 10 ; ; ; ; ;  
; ORGANISM: Artificial/Unknown ; ; ; ; ;  
; FEATURE: NAME/KEY: misc feature ; ; ; ; ;  
; OTHER INFORMATION: Synthetic ; ; ; ; ;  
; FEATURE: NAME/KEY: SITE ; ; ; ; ;  
; LOCATION: (1). (1) ; ; ; ; ;  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline. ; ; ; ; ;  
; FEATURE: NAME/KEY: SITE ; ; ; ; ;  
; LOCATION: (1). (3) ; ; ; ; ;  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline. ; ; ; ; ;  
; FEATURE: NAME/KEY: SITE ; ; ; ; ;  
; LOCATION: (5). (6) ; ; ; ; ;  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline. ; ; ; ; ;  
; US-10-437-708-165 ; ; ; ; ;

Query Match 55.6%; Score 30; DB 17; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRPPL 10 ; ; ; ; ;  
Db 3 PRPPL 7 ; ; ; ; ;

RESULT 8 ; ; ; ; ;  
US-08-344-824-273 ; ; ; ; ;  
; Sequence 273, Application US/08344824  
; Publication No. US20030152580A1 ; ; ; ; ;  
; GENERAL INFORMATION ; ; ; ; ;  
; APPLICANT: SETTE, Alessandro ; ; ; ; ;  
; ATTORNEY/AGENT INFORMATION: SITTE, John ; ; ; ; ;  
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES ; ; ; ; ;  
; NUMBER OF SEQUENCES: 399 ; ; ; ; ;  
; CORRESPONDENCE ADDRESS: ; ; ; ; ;  
; ADDRESSEE: Townsend and Townsend Khourie and Crew ; ; ; ; ;  
; STREET: One Market Plaza, Steuart Street Tower, 20th ; ; ; ; ;  
; STREET: Floor ; ; ; ; ;  
; CITY: San Francisco ; ; ; ; ;  
; STATE: California ; ; ; ; ;  
; COUNTRY: USA ; ; ; ; ;  
; ZIP: 94105 ; ; ; ; ;  
; COMPUTER READABLE FORM: ; ; ; ; ;  
; MEDIUM TYPE: Floppy disk ; ; ; ; ;  
; COMPUTER: IBM PC compatible ; ; ; ; ;  
; OPERATING SYSTEM: PC DOS/MS-DOS ; ; ; ; ;  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 ; ; ; ; ;  
; CURRENT APPLICATION DATA: ; ; ; ; ;  
; APPLICATION NUMBER: US/08/344,824 ; ; ; ; ;  
; FILING DATE: 23-NOV-1994 ; ; ; ; ;  
; CLASSIFICATION: 514 ; ; ; ; ;  
; PRIOR APPLICATION DATA: ; ; ; ; ;  
; APPLICATION NUMBER: US 08/278,634 ; ; ; ; ;  
; FILING DATE: 21-JUL-1994 ; ; ; ; ;  
; ATTORNEY/AGENT INFORMATION: ; ; ; ; ;  
; NAME: Bastian, Kevin L. ; ; ; ; ;  
; REGISTRATION NUMBER: 34,774 ; ; ; ; ;  
; REFERENCE/DOCKET NUMBER: 14137-80-1 ; ; ; ; ;  
; TELECOMMUNICATION INFORMATION: ; ; ; ; ;  
; TELEPHONE: (415) 543-9600 ; ; ; ; ;  
; TELEFAX: (415) 543-5043 ; ; ; ; ;  
; INFORMATION FOR SEQ ID NO: 273: ; ; ; ; ;  
; SEQUENCE CHARACTERISTICS: ; ; ; ; ;  
; LENGTH: 9 amino acids ; ; ; ; ;  
; TYPE: amino acid ; ; ; ; ;  
; STRANDEDNESS: single ; ; ; ; ;  
; TOPOLOGY: linear ; ; ; ; ;  
; MOLECULE TYPE: DNA ; ; ; ; ;  
; US-08-344-B24-273 ; ; ; ; ;

Query Match 51.9%; Score 28; DB 8; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.5e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTRPPL 10 ; ; ; ; ;  
Db 1 DPTRPPL 6 ; ; ; ; ;

RESULT 7 ; ; ; ; ;  
US-10-257-199-165 ; ; ; ; ;  
; Sequence 165, Application US/10257199  
; Publication No. US20040230032A1 ; ; ; ; ;  
; GENERAL INFORMATION ; ; ; ; ;  
; APPLICANT: Kielisiewski, Marcia ; ; ; ; ;  
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
; FILE REFERENCE: ONU-06319 ; ; ; ; ;  
; CURRENT APPLICATION NUMBER: US/10/257,199 ; ; ; ; ;  
; CURRENT FILING DATE: 2003-05-09 ; ; ; ; ;  
; PRIORITY APPLICATION NUMBER: 09/547,693 ; ; ; ; ;  
; NUMBER OF SEQ ID NOS: 244 ; ; ; ; ;  
; SOFTWARE: PatentIn version 3.0 ; ; ; ; ;  
; SEQ ID NO 165 ; ; ; ; ;  
; LENGTH: 10 ; ; ; ; ;  
; TYPE: PRPPL 10 ; ; ; ; ;  
; ORGANISM: Artificial Sequence ; ; ; ; ;  
; FEATURE: ; ; ; ; ;  
; OTHER INFORMATION: Synthetic ; ; ; ; ;  
; NAME/KEY: SITE ; ; ; ; ;

RESULT 9  
US-08-344-824-381  
; Sequence 381, Application US/08344824  
; GENERAL INFORMATION:  
; APPLICANT: SETTE, Alessandro  
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 399  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: Townsend and Townsend Khourie and Crew  
; STREET: One Market Plaza, Steuart Street Tower, 20th  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/344, 824  
; FILING DATE: 23-NOV-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/278, 634  
; FILING DATE: 21-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 14137-80-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5943  
; INFORMATION FOR SEQ ID NO: 381:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-344-824-381

Query Match 51.9%; Score 28; DB 8; Length 10;  
Best Local Similarity 83.3%; Pred. No. 6.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPPL 10  
Db 1 DPTPPL 6

RESULT 10  
US-09-758-128-20  
; Sequence 20, Application US/09758128  
; Patent No. US20020107187A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRITY, No. US20020107187Alman L.  
; TITL OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194, 218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PNP9990  
; PRIOR FILING DATE: 1996-05-22

PRIOR APPLICATION NUMBER: AU PNP9990  
; PRIOR FILING DATE: 1996-05-22

RESULT 11  
US-09-758-128-23  
; Sequence 23, Application US/09758128  
; Patent No. US20020107187A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERBARY, No. US20020107187Alman L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITL OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT FILING NUMBER: US/09/758, 128  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194, 218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PNP9990  
; PRIOR FILING DATE: 1996-05-22

PRIOR APPLICATION NUMBER: AU PNP9990  
; PRIOR FILING DATE: 1996-05-22

RESULT 12  
US-09-758-128-26  
; Sequence 26, Application US/09758128  
; Patent No. US20020107187A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRITY, No. US20020107187Alman L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITL OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT FILING NUMBER: US/09/758, 128  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194, 218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PNP9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 8  
; TYPE: PRT

; ORGANISM: Mouse  
; US-09-758-128-26

Query Match 50.0%; Score 27; DB 9; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0;  
Gaps 0;

Qy 3 AMDPTPPL 10  
Db 1 AISPTPAL 8

RESULT 13  
US-09-758-128-29  
; Sequence 29, Application US/09758128  
; Patent No. US20020107187A1

; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020107187A1man L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,128  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PNR9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 8  
; TYPE: PRT

; ORGANISM: Rat  
; US-09-758-128-29

Query Match 50.0%; Score 27; DB 9; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0;  
Gaps 0;

Qy 3 AMDPTPPL 10  
Db 1 AISPTPAL 8

RESULT 14  
US-09-758-426-20

; Sequence 20, Application US/09758426  
; Patent No. US20020109116A1

; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020109116A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,426  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PNR9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 8  
; TYPE: PRT

; ORGANISM: Porcine  
; US-09-758-426-23

Query Match 50.0%; Score 27; DB 9; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0;  
Gaps 0;

Qy 3 AMDPTPPL 10  
Db 1 AISPTPAL 8

RESULT 14  
US-09-758-426-20

; Sequence 20, Application US/09758426  
; Patent No. US20020109116A1

; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020109116A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,426  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PNR9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 8  
; TYPE: PRT

; ORGANISM: Bovine  
; US-09-758-426-20

Query Match 50.0%; Score 27; DB 9; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.5e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0;  
Gaps 0;

Qy 3 AMDPTPPL 10  
Db 1 AISPTPAL 8

Search completed: January 6, 2005, 11:02:39

Job time : 142 secg  
; ORGANISM: Mouse  
; US-09-758-128-26

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 6, 2005, 10:40:33 ; Search time 37 Seconds  
(without alignments)  
17.924 Million cell updates/sec

Title: US-10-047-945-1  
Perfect score: 54  
Sequence: 1 LKAMDPPTPL 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 110780

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*\*

- 1: /cgmn\_2\_6\_ptodata/l/iaa/5A\_COMB.pep:\*\*
- 2: /cgmn\_2\_6\_ptodata/l/iaa/5B\_COMB.pep:\*\*
- 3: /cgmn\_2\_6\_ptodata/l/iaa/6A\_COMB.pep:\*\*
- 4: /cgmn\_2\_6\_ptodata/l/iaa/6B\_COMB.pep:\*\*
- 5: /cgmn\_2\_6\_ptodata/l/iaa/PCTUS\_COMB.pep:\*\*
- 6: /cgmn\_2\_6\_ptodata/l/iaa/backfles1.pep:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	54	100.0	10	US-08-657-163A-2
2	30	55.6	6	US-09-232-446B-24
3	30	55.6	8	US-09-547-693-168
4	30	55.6	10	US-09-547-693-165
5	27	50.0	6	US-07-983-290-2
6	27	50.0	6	US-08-271-98-2
7	27	50.0	6	US-08-468-996-2
8	27	50.0	6	US-09-293-961-12
9	27	50.0	6	US-09-295-46B-15
10	27	50.0	6	US-09-551-737C-15
11	27	50.0	6	US-09-293-924B-2
12	27	50.0	6	US-09-551-738B-12
13	27	50.0	7	US-07-983-290-3
14	27	50.0	7	US-08-271-698-3
15	27	50.0	7	US-08-468-596-3
16	27	50.0	7	US-09-295-96B-13
17	27	50.0	7	US-09-295-846B-16
18	27	50.0	7	US-09-551-737C-16
19	27	50.0	7	US-09-293-924B-3
20	27	50.0	7	US-09-551-738B-13
21	27	50.0	8	US-07-983-290-4
22	27	50.0	8	US-08-271-698-4
23	27	50.0	8	US-08-468-596-4
24	27	50.0	8	US-09-295-96B-14
25	27	50.0	8	US-09-295-846B-17
26	27	50.0	8	US-09-551-737C-17
27	50.0	8	US-09-295-924B-4	

**ALIGNMENTS**

---

RESULT 1  
US-08-657-163A-2

```

; Sequence 2, Application US/08657163A
; Patent No. 574449
; GENERAL INFORMATION:
; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
; TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIE V. LIPPS
; STREET: 4509 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE: 10 MAY 1993
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N
;
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; ORIGINAL SOURCE: SYNTHETIC  
; US-08-657-163A-2

Query Match 100.0%; Score 54; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.004; Mismatches 0;  
Matches 10; Conservative 0; Indels 0; Gaps 0;

Qy	1 LKAMDPPTPL 10	Db	1 LKAMDPPTPL 10
----	-----------------	----	-----------------

RESULT 2  
US-09-232-446B-24  
Sequence 24, Application US/09232446B  
; Patent No. 622647  
GENERAL INFORMATION:  
APPLICANT: Vortex, Daniel F.  
APPLICANT: Gai, Xiaolu  
TITLE OF INVENTION: Transposable Element Protein that Directs DNA  
TITLE OF INVENTION: Integration to Specific Chromosomal Site  
FILE REFERENCE: 2-98  
CURRENT APPLICATION NUMBER: US/09/232,446B  
CURRENT FILING DATE: 1999-01-15  
PRIORITY APPLICATION NUMBER: US 60/071,383  
PRIORITY FILING DATE: 1998-01-15  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 24  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: mutant peptide

US-09-232-446B-24

Query Match 55.6%; Score 30; DB 3; Length 6;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	4 MDPPTP 9	Db	1 LDPSPP 6
----	------------	----	------------

RESULT 3  
US-09-547-693-168  
Sequence 168, Application US/09547693  
; GENERAL INFORMATION:  
; Patent No. 6339050  
; APPLICANT: Kieliszewski, Marcia  
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
FILE REFERENCE: OHU-04089  
CURRENT APPLICATION NUMBER: US/09/547,693  
NUMBER OF SEQ ID NOS: 236  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 165  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial/Unknown  
FEATURE:  
NAME/KEY: misc feature  
NAME/KEY: misc feature  
OTHER INFORMATION: Synthetic  
NAME/KEY: SITE  
LOCATION: (1)..(1)  
OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
NAME/KEY: SITE  
LOCATION: (3)..(3)  
OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
NAME/KEY: SITE  
LOCATION: (5)..(6)  
OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

US-09-547-693-168

Query Match 55.6%; Score 30; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 39; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6 PTTPPL 10	Db	3 PTTPPL 7
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RESULT 5  
US-07-989-290-2  
Sequence 2, Application US/07989290  
; Patent No. 5358934  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov  
; APPLICANT: Carlson, David A.  
TITLE OF INVENTION: Materials and Methods for Control  
TITLE OF INVENTION: Of Pests  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Salivanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DO/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

US-09-547-693-168

; LOCATION: (1)..(1)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Synthetic  
NAME/KEY: SITE  
LOCATION: (3)..(4)  
OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

US-09-547-693-168

APPLICATION NUMBER: US/07/989,290 ; HYPOTHETICAL: NO  
 FILING DATE: 1992-11-21 ; ANTI-SENSE: NO  
 CLASSIFICATION: 435 ; US-08-271-698-2  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: UP/S&S-127  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-8800  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: AMINO ACID  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-07-989-290-2

RESULT 6  
 US-08-271-698-2 Application US/08271698  
 Sequence 2, Application US/08271698  
 Patent No. 5439821  
 GENERAL INFORMATION:  
 APPLICANT: Borovsky, Dov  
 TITLE OF INVENTION: Materials and Methods for Control  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: USA  
 ZIP: 32606

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/468,596  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/271,698  
 FILING DATE: 07-JUL-1994  
 APPLICATION NUMBER: US/07/989,290  
 FILING DATE: 11-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: UP/S&S-127  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-468-596-2

RESULT 7  
 US-08-468-596-2  
 Sequence 2, Application US/08468596  
 Patent No. 5629196  
 GENERAL INFORMATION:  
 APPLICANT: Carlson, David A.  
 TITLE OF INVENTION: Materials and Methods for Control  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: USA  
 ZIP: 32606

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/468,596  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/271,698  
 FILING DATE: 07-JUL-1994  
 APPLICATION NUMBER: US/07/989,290  
 FILING DATE: 11-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: UP/S&S-127  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-468-596-2

RESULT 8  
 US-09-295-996B-12

APPLICATION NUMBER: US/07/989,290 ; HYPOTHETICAL: NO  
 FILING DATE: 1992-11-21 ; ANTI-SENSE: NO  
 CLASSIFICATION: 435 ; US-08-271-698-2  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: UP/S&S-127  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-8800  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-07-989-290-2

```

; Sequence 12, Application US/09295996B
; Patent No. 6413330
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UP-230
; CURRENT APPLICATION NUMBER: US/09/295,996B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
; US-09-295-996B-12

Query Match      50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      5 DPTPP 9
Db      2 DPAPP 6

RESULT 9
US-09-295-846B-15
; Sequence 15, Application US/09295846B
; Patent No. 6562590
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UP-223
; CURRENT APPLICATION NUMBER: US/09/295,846B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF peptide
; US-09-295-846B-15

Query Match      50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      5 DPTPP 9
Db      2 DPAPP 6

RESULT 10
US-09-551-737C-15
; Sequence 15, Application US/09551737C
; Patent No. 6566129
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Schlesinger, Yaakov
; APPLICANT: Naueelaars, Sabine M. I.
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UP-223C1
; CURRENT APPLICATION NUMBER: US/09/551,737C
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
; US-09-551-737C-15

Query Match      50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      5 DPTPP 9
Db      2 DPAPP 6

RESULT 11
US-09-295-924B-2
; Sequence 2, Application US/09295924B
; Patent No. 6593299
; GENERAL INFORMATION:
; APPLICANT: John, Bennett
; APPLICANT: Alan, Brandt
; APPLICANT: Dov, Borovsky
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROLLING PESTS
; FILE REFERENCE: 4137-120
; CURRENT APPLICATION NUMBER: US/09/295,924B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: Truncated TMOF
; US-09-295-924B-2

Query Match      50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      5 DPTPP 9
Db      2 DPAPP 6

RESULT 12
US-09-551-738B-12
; Sequence 12, Application US/09551738B
; Patent No. 6635255
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae
; FILE REFERENCE: UP-224C1
; CURRENT APPLICATION NUMBER: US/09/551,738B
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/296,113
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
; US-09-551-738B-12

Query Match      50.0%; Score 27; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      5 DPTPP 9
Db      2 DPAPP 6

```

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPTRP 9  
Db 2 DPAPP 6

RESULT 13  
US-07-989-290-3  
; Sequence 3, Application US/07989290  
; Patent No. 535934  
; GENERAL INFORMATION:  
; TITLE OF INVENTION: Materials and Methods for Control  
; TITLE OF INVENTION: of Pests  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
ZIP: 32606

COMPUTER READABLE FORM:  
COMPUTER: Floppy disk  
COMPILER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/271,698  
FILING DATE: 07-JUL-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/07/989,290  
FILING DATE: 11-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE DOCKET NUMBER: UF/S&S-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 3:  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTER NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: UF/S&S-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800

SEQUENCE CHARACTERISTICS:  
SEQUENCE NUMBER: US/07/989,290  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

US-07-989-290-3

RESULT 14  
US-08-271-698-3  
; Sequence 3, Application US/08271698  
; Patent No. 5439621  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov A.  
; TITLE OF INVENTION: Materials and Methods for Control  
; TITLE OF INVENTION: of Pests  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
ZIP: 32606

COMPUTER READABLE FORM:  
COMPUTER: Floppy disk  
COMPILER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,596  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/271,698  
FILING DATE: 07-JUL-1994  
APPLICATION NUMBER: US/07/989,290

RESULT 15  
US-08-468-596-3  
; Sequence 3, Application US/08468596  
; Patent No. 5622196  
; GENERAL INFORMATION:  
; APPLICANT: Borovsky, Dov A.  
; TITLE OF INVENTION: Materials and Methods for Control  
; TITLE OF INVENTION: of Pests  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
ZIP: 32606

COMPUTER READABLE FORM:  
COMPUTER: Floppy disk  
COMPILER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,596  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/271,698  
FILING DATE: 07-JUL-1994  
APPLICATION NUMBER: US/07/989,290

PILING DATE: 11-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: UP/S&S-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-468-596-3

Query Match 50.0%; Score 27; DB 1; Length 7;  
Best Local Similarity 80.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 DPTPP 9  
Db 2 DPAPP 6

Search completed: January 6, 2005, 10:51:59  
Job time : 38 SECs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: January 6, 2005, 10:59:50 ; Search time 38 Seconds  
(without alignments)  
37.980 Million cell updates/sec

Title: US-10-047-945-2  
Perfect score: 84  
Sequence: 1 LKAMDPPTPLWIKTB 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched:  
283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Listing First 45 summaries

Database : PIR\_79;\*  
1: pir1;\*  
2: pir2;\*  
3: pir3;\*  
4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	27	32.1	7 2	A61081
2	27	32.1	10 2	A36554
3	27	32.1	15 2	A47628
4	25	29.8	13 2	PI1620
5	25	29.8	15 2	PD0444
6	24	28.6	8 2	S21288
7	23	27.4	7 4	A58723
8	23	27.4	12 2	I58273
9	23	27.4	15 2	B39109
10	23	27.4	15 2	B6157
11	22	26.2	13 2	G3756
12	22	26.2	13 2	D37567
13	22	26.2	14 2	PT0026
14	22	26.2	15 2	PT0037
15	21	25.0	10 2	C35589
16	21	25.0	10 2	B59274
17	21	25.0	10 2	S39030
18	21	25.0	11 1	XAVIER
19	21	25.0	11 2	C59151
20	21	25.0	15 2	PA0055
21	21	25.0	15 2	A26212
22	20	23.8	21 2	B60274
23	20	23.8	8 2	S10783
24	20	23.8	8 2	A39308
25	20	23.8	9 2	S78422
26	20	23.8	12 1	JTJGO
27	20	23.8	12 2	PN0663
28	20	23.8	14 2	FH1448
29	20	23.8	14 2	A60158

## ALIGNMENTS

RESULT 1  
A61081  
t-Tryptophyllin, basic - Robde's leaf frog

C.SpeciesB: Phylomedusa rodrigi (Robde's leaf frog)  
C.Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000

R.Montecuccini, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Brspanier, V.

Int. J. Pept. Protein Res. 33, 391-395, 1989

A.Title: Isolation, structure determination and synthesis of a novel tryptophan-contain

A.Reference number: A61081

A.Molecule type: protein

A.Residues: 1-7 <MON>

C.Comment: The biological activity of this peptide was not determined.

C.Superfamily: unassigned animal peptide

C.Keywords: amidated carboxyl end; hydroxyproline; skin

F7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 32.1%; Score 27; DB 2; Length 7;

Best Local Similarity 80.0%; Pred. No. 2.8e+05; Matches 4; Conservative 0; Mismatches 1; Indels 0; Caps 0;

Qy	8 PPRWI 12
Db	2 PRSWI 6

RESULT 2  
A61454

tryptophyllin, basic - Robde's leaf frog

trypsin-modulating

FC gamma receptor

Ig H chain V-D-J R

coupling factor 6 (f

lectin - potato

virotoxin - destro

thyroglobulin - ra

hypothetical 1.5K

alpha-glucosidase

ig heavy chain C r

C-Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-Jul-2004

C.Species: Aedes aegypti (Yellow fever mosquito)

R.Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

FASEB J. 4, 3015-3020, 1990

A.Title: Mosquito oobatic factor: a novel decapeptide modulating trypsin-like enzyme b

A.Reference number: A36454; MUID:9036788; PMID:2394318

A.Molecule type: protein

A.Residues: 1-10 <BOR>

A.Cross-references: UNIPROT:P19425

R.Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

A.Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oob. major protein anti-enamelin F - bovin glycine reductase 52.5K protein - sp tremogen A-10 - dytrophin-abscia Ig heavy chain DJ disaggregatase

A.Reference number: A61630; MUID:9335794; PMID:8353526

A.Accession: A61630

A.Molecule type: protein

A.Residues: 1-10 <BO2>

A.Note: none of the amino acids is modified

C.Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ei

C;Keywords: hormone

Query Match 32.1%; Score 27; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.8e+02; 0; Mismatches 4; Conservative 1; Indels 0; Gaps 0;

Matches 4;

Qy 5 DPTPP 9

Db 2 DPAPP 6

RESULT 3

A47628

Fc gamma receptor II (CD32) - human (fragments)

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C;Accession: A47628

R;Warmerdam, P.M.; van de Winkel, J.G.J.; Gosselin, B.J.; Capel, P.J.A.

J. Exp. Med. 172, 19-25, 1990

A;Title: Molecular basis for a polymorphism of human Fc gamma receptor II (CD32).

A;Reference number: A47628; PMID:9293679; PMID:2141627

A;Accession: A47628

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-15 &lt;WAR&gt;

C;Keywords: immunoglobulin receptor

Query Match 32.1%; Score 27; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 2.8e+02; 0; Mismatches 4; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MDPPPLW 11

Db 1 MTAAPPCW 8

RESULT 4

PH1620

Ig H chain V-D-J region (clone B-less 40) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1620

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Biol. Med. 78, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1620; PMID:93301609; PMID:8315387

A;Molecule type: DNA

A;Residues: 1-13 &lt;LEV&gt;

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 29.8%; Score 25; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 5e+02; 0; Mismatches 4; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 7 TPPMLW 11

Db 8 TPKMLW 12

RESULT 5

PD0444

coupling factor 6 mitochondrial - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 05-Feb-1999

C;Accession: PD0444

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morinaga, T.; Tsugita, A.

submitted to JIPB, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Content: Striatum

A;Accession: PD0444

A;Molecule type: protein

A;Residues: 1-15 &lt;RAW&gt;

C;Keywords: mitochondrion

Query Match 29.8%; Score 25; DB 2; Length 15;

Best Local Similarity 36.4%; Pred. No. 5.8e+02; 0; Mismatches 4; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KAMDPPPPMI 12

Db 2 KELDPVQKLFLV 12

RESULT 6

S21288

lectin - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Accession: S21288 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004

R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.

Biochem. J. 263, 813-821, 1992

A;Title: Chitin-binding proteins in potato (*Solanum tuberosum* L.) tuber. Characterization

A;Reference number: S21288; PMID:92272683; PMID:1590771

A;Accession: S21288

A;Molecule type: protein

A;Residues: 1-8 &lt;WIL&gt;

A;Cross-references: UNIPROT:Q7MLV6

C;Function:

A;Description: may be involved in defence mechanism of the plant

C;Keywords: hydroxyproline; lectin

Query Match 28.6%; Score 24; DB 2; Length 8;

Best Local Similarity 57.1%; Pred. No. 2.8e+05; 0; Mismatches 2; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPPPP 9

Db 2 ASTPSPP 8

RESULT 7

A58725

Virotoxin - destroying angel

C;Species: Amanita virosa (destroying angel)

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C;Accession: A58725

R;Failliech, H.; Bokku, A.; Bodenmuller, H.; Wieland, T.

Biochemistry 19, 334-343, 1980

A;Title: Virotoxins: actin-binding cyclic peptides of *Amanita virosa* mushrooms.

A;Reference number: A58725; PMID:6893271; PMID:6893271

A;Accession: A58725

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 &lt;PAU&gt;

C;Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide

F;1-/Cross-link: cyclopeptide (Val-leu) #status experimental

F;2/Modified site: D-threonine (Thr) #status experimental

F;3/Modified site: D-serine (Ser) #status experimental

F;4/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental

F;5/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental

F;7/Modified site: 4,5-dihydroxyleucine (Leu) #status experimental

Query Match 27.4%; Score 23; DB 4; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+02; 0; Mismatches 3; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TPPMLW 12

Db 2 TSPAWL 7

RESULT 8

158273 thyroglobulin - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: 158273  
R;Musci, A.M.; Urbini, V.M.; Avvedimento, E.V.; Zimarino, V.; Di Lauro, R.  
Nucleic Acids Res. 15, 819-8166, 1987  
A;Title: A cell type specific factor recognizes the rat thyroglobulin promoter.  
A;Reference number: 158273; MUID: 8804046; PMID: 3671079  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Residues: 1-12 <RES>  
A;Cross-references: UNIPROT:Q63579; EMBL:X06162; NID:957368; PIDN:CAA29519.1; PID:957369  
Query Match 27.4%; Score 23; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 TPPL 10  
Db 6 TPPL 9  
RESULT 9  
B39109 hypothetical 1.5K protein - hepatitis C virus  
N;Alternate name: hypothetical protein 2  
C;Species: hepatitis C virus  
C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
C;Accession: B39109; JQ1585  
R;Han, J.H.; Shymala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-O'Toole, M.A.; Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identification of a poly-A tail  
A;Reference number: A39109; MUID: 9156678; PMID: 1705704  
A;Accession: B39109  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residue: 1-15 <RAN>  
A;Cross-references: GB:M58406  
R;Kumar, Y.; Cheng, D.; Thomas, H.; Monjardino, J.  
J. Gen. Virol. 73, 1521-1525, 1992  
A;Title: Cloning and sequencing of the structural region and expression of putative core protein genes of hepatitis C virus  
A;Reference number: JQ1584; MUID: 92300349; PMID: 1318944  
A;Accession: JQ1585  
A;Molecule type: genomic RNA  
A;Residues: 1-15 <KUM>  
A;Experimental source: strain U.K.  
Query Match 27.4%; Score 23; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 6 PTPL 10  
Db 7 PGPL 11  
RESULT 10  
B61457 alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)  
C;Species: Tetrahymena pyriformis  
C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999  
C;Accession: B61457  
R;Barroso, Y.; Sasaki, N.; Yoshihiko, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.  
J. Protozool. 36, 562-567, 1989  
A;Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification and characterization  
A;Reference number: B61457; MUID: 90095988; PMID: 2689637  
A;Accession: B61457  
A;Molecule type: protein  
A;Residue: 1-15 <BAN>  
A;Genetic code: SGCS  
Query Match 26.2%; Score 22; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 PLW 11  
Db 10 PLW 12  
RESULT 11  
G37266 Ig heavy chain C region (Py2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
C;Accession: G37266  
R;Ruff, Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6007-6013, 1991  
A;Title: Heavy and light chain variable region sequences and antibody properties of anti-Ig heavy chain  
A;Reference number: A18740; MUID: 91177923; PMID: 1706720  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-13 <RUF>  
A;Accession: G37266  
A;Molecule type: mRNA  
A;Residue: 1-15 <RAN>  
A;Cross-references: GB:M58406  
R;Urbano, Y.; Sasaki, N.; Yoshihiko, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.  
J. Protozool. 36, 562-567, 1989  
A;Title: Cloning and sequencing of the structural region and expression of putative core protein genes of hepatitis C virus  
A;Reference number: JQ1584; MUID: 92300349; PMID: 1318944  
A;Accession: JQ1585  
A;Molecule type: genomic RNA  
A;Residues: 1-15 <KUM>  
A;Experimental source: strain U.K.  
Query Match 26.2%; Score 22; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 PLW 11  
Db 10 PLW 12  
RESULT 12  
D37267 Ig heavy chain C region (Py69) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
C;Accession: D37267  
R;Ruff, Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 266, 6007-6013, 1991  
A;Title: Heavy and light chain variable region sequences and antibody properties of anti-Ig heavy chain  
A;Reference number: A18740; MUID: 91177923; PMID: 1706720  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-13 <RUF>  
A;Accession: D37267  
A;Molecule type: mRNA  
A;Residue: 1-15 <RAN>  
A;Cross-references: GB:M58406  
R;Urbano, Y.; Sasaki, N.; Yoshihiko, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.  
J. Protozool. 36, 562-567, 1989  
A;Title: Cloning and sequencing of the structural region and expression of putative core protein genes of hepatitis C virus  
A;Reference number: JQ1584; MUID: 92300349; PMID: 1318944  
A;Accession: JQ1585  
A;Molecule type: genomic RNA  
A;Residues: 1-15 <KUM>  
A;Experimental source: strain U.K.  
Query Match 26.2%; Score 22; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 PLW 11  
Db 10 PLW 12  
RESULT 13  
PT0026 calotropin DI - mudar (fragment)  
C;Species: Calotropis gigantea (mudar, madar)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: PT0026  
R;Bhattacharya, D.; Sengupta, A.; Sinha, N.K.  
Phytochem. 26, 633-636, 1987  
A;Title: Chemical modification and amino terminal sequence of calotropin DI from Calotropis gigantea  
A;Reference number: PT0026  
A;Accession: PT0026  
A;Molecule type: protein  
A;Residues: 1-14 <BHA>  
A;Cross-references: UNIPROT:P20728

C;Comment: This enzyme is classified as a plant cysteine protease.  
 C;Keywords: pyroglutamic acid  
 P;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental

Query Match 26.2%; Score 22; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.7e-03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PTPLW 11  
 Db 3 PEYPW 8

## RESULT 14

PT0037 light harvesting complex chain III/b, photosystem I - rice (fragment)

C;Species: Oryza sativa (rice)  
 C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004

C;Accession: PT0037; PS0205  
 R.Uchiyama, Y.; Tsugita, A.  
 submitted to JIPID, June 1991

A;Reference number: PS0189

A;Accession: PT0037  
 A;Molecule type: protein  
 A;Residues: 1-15 <UCH>  
 A;Cross-references: UNIPROT:Q7MIV1

Query Match 26.2%; Score 22; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDPTPP 9  
 Db 4 EAAPP 11

## RESULT 15

C35389 urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)

C;Species: Morganella morganii  
 C;Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 09-Jul-2004

C;Accession: C35389  
 R.Hu, L.T.; Nicholson, B.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J.Bacteriol. 172, 3073-3080, 1990  
 A;Title: Morganella morganii urease: purification, characterization, and isolation of gene

A;Reference number: A35389; MUID:90264298; PMID:2345135

A;Accession: C35389  
 A;Status: preliminary

A;Molecule type: protein  
 A;Residues: 1-10 <HUA>  
 A;Cross-references: UNIPROT:P17339

C;Keywords: hydrolase

Query Match 25.0%; Score 21; DB 2; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MDPPPP 9  
 Db 1 MQLTPP 6

Search completed: January 6, 2005, 11:09:13  
 Job time : 40 secs

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GenCore version 5.1.2

OM protein - protein search, using sw model

Run on: January 6, 2005, 10:52:04 ; Search time 189 Seconds  
 (without alignment(s))  
 45.908 Million cell updates/sec

Total number of hits satisfying chosen parameters:	7754			
Minimum DB seq length:	0			
Maximum DB seq length:	15			
Post-processing:	Minimum Match 0%			
	Maximum Match 100%			
Database :	UniProt 02.*			
	1: uniprot_sprot:*			
	2: uniprot_trembl:*			
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	27	32.1	7	TPPFY_PACDA
2	27	32.1	10	TMOP_AEDAE
3	27	32.1	14	Q96P2
4	26	31.0	11	Q9UERI
5	25	29.8	12	Q6XV6I
6	25	29.8	12	Q8KZ86
7	25	29.8	12	AAP79619
8	25	29.8	13	BCD8_LYMD1
9	25	29.8	14	Q9TEN1
10	25	29.8	14	Q9TEN3
11	24	28.6	8	Q7MIV6
12	24	28.6	14	Q6SE52
13	24	28.6	14	AAR23007
14	23	27.4	10	Q76MK5
15	23	27.4	10	BAB87160
16	23	27.4	11	Q8TG8
17	23	27.4	11	CAA33464
18	23	27.4	12	Q65P79
19	23	27.4	14	TAT_HV1W2
20	23	27.4	14	TAT_HV128
21	23	27.4	14	Q8HR43
22	23	27.4	14	Q8JDM0
23	23	27.4	14	Q8JDN7
24	23	27.4	14	Q8JDM3
25	23	27.4	14	AAL78488
26	22	26.2	11	Q8M21
27	22	26.2	11	Q8M23
28	22	26.2	11	Q8MB39
29	22	26.2	11	Q8MB58
30	22	26.2	11	Q8MB77
31	22	26.2	11	Q8MB79

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Title: US-10-047-945-2

Sequence: 1 LKANDPTPRWIKR 15

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1	TPPFY_PACDA	STANDARD;	PRT;	7 AA.
ID	TPPFY_PACDA			
AC	P81455;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DB	Tryptophyllin-1 (Pdt-1)			
OS	Pachymedusa dacnicolor (Giant mexican leaf frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;			
OX	Phylomedusinae; Pachymedusa.			
RN	[1] NCBI_TAXID=75988;			
RP	SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF PRO-7.			
RP	TISSUE-SKIN secretion;			
RA	Chen T.B., Orr D.F., Shaw C.;			
RT	"Pachymedusa dacnicolor tryptophyllin-1 (Pdt-1); structural characterization, pharmacological activity and cloning of precursor			
RT	CDNA;"			
RL	Submitted (SBP-2002) to Swiss-Prot.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Skin.			
CC	-1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref. 1.			
DR	GO: GO:0005576; C:extracellular; NAS.			
DR	GO: GO:0045986; P:negative regulation of smooth muscle contraction; NAS.			
KW	Amidation; Amphibian defense peptide; Direct protein sequencing; KW Hydroxylation.			
KW	Hydroxylation.			
FT	MOD_RES 3			
FT	MOD_RES 7			
FT	SEQUENCE 7 AA: 794 MW: 7772037DC776350 CRC64;			
Query Match	32.1%; Score 27; DB 1; Length 7;			
Best Local Similarity	60.0%; Pred. No. 1.8e+06;			
Matches	1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	8 PPIWI 12			
Db	2 PPAWV 6			

RESULT 2

TMOP_AEDAE	STANDARD;	PRT;	10 AA.
ID	TMOP_AEDAE		
AC	P13425;		
DT	01-NOV-1990 (Rel. 16, Created)		
DT	01-NOV-1990 (Rel. 16, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DB	Trypsin-modulating oostactic factor (TMOP) (OOSH).		
OS	Acetes aegypti (Yellowfever mosquito).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		

ALIGNMENTS

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
 OC NCBI\_TaxID=7159;  
 RN [1]  
 RP SQUENCE.  
 RC STRAIN="Vero beach; TISSUE=Ovary;  
 RX RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
 RT RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like  
 enzyme biosynthesis in the midgut.,";  
 PASEB J. 4:3015-3020(1990).  
 RN [2]  
 RP SQUENCE.  
 RC STRAIN="vero beach; TISSUE=Ovary;  
 RX MEDLINE=9335794; PubMed=8353526;  
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
 RT RT "Mass spectrometry and characterization of *Aedes aegypti* trypsin  
 modulating oostatic factor (TMOF) and ITB analogs.,";  
 RL Insect Biochem. Mol. Biol. 23:703-712(1993).  
 CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis  
 in the midgut which indirectly reduces the vitellogenin  
 concentration in the hemolymph resulting in inhibition of oocyte  
 development.  
 CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular  
 epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs  
 CC and stops at 56 hrs.  
 DR PIR; A36454; A36454;  
 KW Direct protein sequencing; Hormone.  
 FT VARIANT 1 2 YD -> DY IN TMFO(B1);  
 DOMAIN 3 10 236DDA7777776DC7 CRC64;  
 SEQUENCE 10 AA; 1047 MW;

Query Match 32.1%; Score 27; DB 1; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+03; Mismatches 1; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; MisMatches 1; Del 0; Insert 0; Gap 0;

Qy 5 DPTRP 9  
 Db 2 DPAPP 6

RESULT 3  
 Q96QP2 PRELIMINARY; PRT; 14 AA.

ID Q96QP2; PRELIMINARY; PRT; 14 AA.  
 AC 096QP2;  
 DT 01-DEC-2001 (TREMBREL 19, Created)  
 DT 01-DEC-2001 (TREMBREL 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBREL 19, Last annotation update)  
 DE Tissue factor pathway inhibitor-2 (Fragment).  
 OS Homo sapiens (Human).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22643823; PubMed=12757776;  
 RA Rube F., Reverdau P., Loehmann S., Cherpi-Antar C., Gruel Y.;  
 RT "Characterization and functional analysis of TPP1-2 gene promoter in a  
 human choriocarcinoma cell line.,";  
 RL Thromb. Res. 109:207-215(2003).  
 DR EMBL; AY044097; AKK72693.1; -.  
 FT NON\_TER 14 14 SQ SEQUENCE FROM N.A.  
 RX MEDLINE=22643823; PubMed=12757776;  
 RA Rube F., Reverdau P., Loehmann S., Cherpi-Antar C., Gruel Y.;  
 RT "Characterization and functional analysis of TPP1-2 gene promoter in a  
 human choriocarcinoma cell line.,";  
 RL Thromb. Res. 109:207-215(2003).  
 DR EMBL; AY044097; AKK72693.1; -.  
 FT NON\_TER 14 14 SQ SEQUENCE FROM N.A.; 1509 MW; 4B70BD6001BC1177 CRC64;

Query Match 32.1%; Score 27; DB 2; Length 14;  
 Best Local Similarity 71.4%; Pred. No. 2.1e+03; Mismatches 2; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; MisMatches 2; Del 0; Insert 0; Gap 0;

Qy 4 MDPTPPL 10  
 Db 1 MDPARPL 7

RESULT 6  
 Q8KZ86 PRELIMINARY; PRT; 12 AA.  
 ID Q8KZ86; PRELIMINARY; PRT; 12 AA.  
 AC Q8KZ86;  
 DT 01-OCT-2002 (TREMBREL 22, Created)  
 DT 01-OCT-2002 (TREMBREL 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBREL 22, Last annotation update)  
 DE Class I integron DNA integrase (Fragment).

Query Match 29.8%; Score 25; DB 2; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 3.6e+03; Mismatches 4; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; MisMatches 4; Del 0; Insert 0; Gap 0;

Qy 4 MDPTPPLW 11  
 Db 1 MSPRPLAW 8

RESULT 6  
 Q8KZ86 PRELIMINARY; PRT; 12 AA.  
 ID Q8KZ86; PRELIMINARY; PRT; 12 AA.  
 AC Q8KZ86;  
 DT 01-OCT-2002 (TREMBREL 22, Created)  
 DT 01-OCT-2002 (TREMBREL 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBREL 22, Last annotation update)  
 DE Class I integron DNA integrase (Fragment).

RESULTS 4

GN	Name=intI1;	RN	[1]
OS	Acinetobacter baumannii.	RP	SEQUENCE.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	RC	TISSUE-Brain;
OX	Moraxellaceae; Acinetobacter.	RX	Medline=97307807; PubMed=243752;
RN	[1]	RA	Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D., Bell R.A.;
RP	SEQUENCE FROM N.A.	RT	"Naturally occurring analogs of Lymantria testis ecdysiotropin, a gonadotropin isolated from brains of Lymantria dispar pupae.";
RX	Medline=2220987; PubMed=12384388;	RL	Arch. Insect Biochem. Physiol. 36:37-50(1997).
RA	Gombac P., Riccio M.L., Rossolini G.M., Lagatolla C., Tonin E., Monti-Bragadin C., Lavenia A., Dolzani L.;	CC	-1- FUNCTION: stimulates synthesis of ecdysteroid in the testes of larvae and pupae.
RT	"Molecular characterization of integrins in epidemiologically unrelated clinical isolates of Acinetobacter baumannii from Italian hospitals reveals a limited diversity of gene cassette arrays.";	KW	Direct protein sequencing.
RT	Antimicrob. Agents Chemother. 46:3665-3668(2002).	SQ	SEQUENCE 13 AA; 1357 MW; 1841B4C3275B764 CRC64;
RL	EMBL; AJ31334; CAC85941.1; -.	Query Match	29.8%; Score 25; DB 1; Length 13;
DR	NON_TER 12 12	Best Local Similarity	66.7%; Pred. No. 3.9e+03;
FT	SEQUENCE 12 AA; 1256 MW; 90426B8P5E376C1 CRC64;	Matches	1; Mismatches 1; Indels 0; Gaps 0;
SQ		QY	3 AMDPTPP 8
Query Match	29.8%; Score 25; DB 2; Length 12;	Db	4 ATAPLPL 11
Best Local Similarity	62.5%; Pred. No. 3.6e+03;		
Matches	5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	3 AMDPTPP 10		
Db	4 ATAPLPL 11		
RESULT 7		RESULT 9	
RA	AAP79619	OPEN1	PRELIMINARY;
ID	AAP79619	OPEN1	PRT;
AC	AAP79619;	OPEN1;	12 AA.
DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)	AC	QTCEN1;
DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Created)
DB	Insulin-like factor 3 (Fragment).	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
GN	INSI3.	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
OS	Canis familiaris (Dog).	DE	ArPasae 8 (Fragment).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OS	Anas castanea (Chestnut teal).
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	OG	Mitochondrion.
OX		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
RN	[1]	OX	NCBI_TaxID=45631;
RP	SEQUENCE FROM N.A.	RN	[1]
RX	PubMed-12890727;	RP	SEQUENCE FROM N.A.
RA	Truong A., Bogatcheva N.V., Schelling C., Dolf G., Agoulnik A.I.;	RA	Kennedy M., Spencer H.G.;
RT	"Isolation and Expression Analysis of the Canine Insulin-Like Factor 3 Gene.";	RT	"Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
RT	Gene. ; Biol. Reprod. 69:1658-1664(2003).	RL	Auk 117:154-163(2000);
RL	Reprod. 69:1658-1664(2003).	DR	Embl; AF173494; Aad51052.1; -.
DR	EMBL; AV251015; AAP79619.1; -.	DR	GO; GO:0005739; C:mitochondrion; IEA.
FT	NON_TER 12 12	FT	Mitochondrion.
SQ	SEQUENCE 12 AA; 1354 MW; 20ED91ADFA7DD737 CRC64;	SQ	SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;
Query Match	29.8%; Score 25; DB 2; Length 12;	Query Match	29.8%; Score 25; DB 2; Length 14;
Best Local Similarity	50.0%; Pred. No. 3.6e+03;	Best Local Similarity	66.7%; Pred. No. 4.3e+03;
Matches	4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Matches	1; Mismatches 2; Indels 0; Gaps 0;
QY	4 MDPPTPLW 11	QY	6 PTPLW 11
Db	1 MSFRPLW 8	Db	6 PTPLW 11
RESULT 8		RESULT 10	
RA	ECDB-LMDI STANDARD	OPENT3	PRELIMINARY;
ID	ECDB-LMDI STANDARD	OPENT3	PRT;
AC	PO0941;	OPENT3	14 AA.
DT	15-JUL-1998 (Rel. 36, Created)	AC	OPENT3;
DT	15-JUL-1998 (Rel. 36, Last sequence update)	DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	05-JUL-2004 (Rel. 44, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DB	Testis ecdisiotropin peptide B (TE).	DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
OS	Lymantria dispar (Gypsy moth).	DE	ArPasae 8 (Fragment).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Globasta; Dipterybia; Noctuoidea;	OS	Anas gracilis (Grey teal).
OC	Lymantidae; Lymantria.	OG	Mitochondrion.
OX	NCBI_TaxID=13123;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
RT	"Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";	OX	NCBI_TaxID=45630;
		RN	[1]
		RP	SEQUENCE FROM N.A.
		RA	Kennedy M., Spencer H.G.;
		RT	"Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";

RL Auk 117:154-163 (2000); Score 24; DB 2; Length 14;  
 DR EMBL; AR173493; AR051050; 1; -; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 1 1  
 SQ SEQUENCEC 14 AA; 1672 MW; 80FB80372F9B871 CRC64;  
 Query Match 29.8%; Score 25; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 4.3e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 6 PTPPLW 11  
 Db 6 PTPWAW 11.

RESULT 11  
 QM1V6 PRELIMINARY; PRT; 8 AA.  
 AC QM1V6;  
 DT 01-MAR-2004 (TREMBrel. 26, Created)  
 DT 01-MAR-2004 (TREMBrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)  
 DB Lectin (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Buharyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiids; Solanales; Solanaceae; Solanum.  
 NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RA Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,  
 RA Bolwell G.P.;  
 RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber."  
 RT Characterization, immunolocalization and effects of wounding.";  
 RL Blochim. J. 283:811-821 (1992).  
 DR PIR: S21288; S21288.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 771 MW; C37775A771B5BDAA CRC64;  
 Query Match 28.6%; Score 24; DB 2; Length 8;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0;  
 QY 3 AMDPPIP 9  
 Db 2 ASTSFPP 8

RESULT 12  
 QSE52 PRELIMINARY; PRT; 14 AA.  
 AC QSE52;  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DB Pgi (Fragment).  
 OS Drosophila simulans (Fruit fly).  
 NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Halligan D.L., Byrne-Walker A., Andolfatto P., Keightley P.D.;  
 RA "Patterns of Evolutionary Constraints in Intronic and Intergenic DNA  
 of Drosophila";  
 RT Genome Res. 14:273-279 (2004).  
 RL EMBL; AY59549; ARX23007; 1; -.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1456 MW; 2C83B49CCD8E7B37 CRC64;  
 Query Match 28.6%; Score 24; DB 2; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 6.1e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 PTPPL 10  
 Db 4 PLPPL 8

RESULT 13  
 AAR23007 PRELIMINARY; PRT; 14 AA.  
 AC AAR23007;  
 DT 02-MAR-2004 (TREMBrel. 27, Created)  
 DT 02-MAR-2004 (TREMBrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBrel. 27, Last annotation update)  
 DB PgI (Fragment).  
 OS Drosophila simulans (Fruit fly).  
 OC Buharyota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriidae; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7240;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Halligan D.L., Byrne-Walker A., Andolfatto P., Keightley P.D.;  
 RA "Patterns of Evolutionary Constraints in Intronic and Intergenic DNA  
 of Drosophila";  
 RT Genome Res. 14:273-279 (2004).  
 RL EMBL; AY59549; ARX23007; 1; -.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1456 MW; 2C83B49CCD8E7B37 CRC64;  
 Query Match 28.6%; Score 24; DB 2; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 6.1e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 PTPPL 10  
 Db 4 PLPPL 8

RESULT 14  
 Q76MKS PRELIMINARY; PRT; 10 AA.  
 AC Q76MKS;  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)  
 DB ATPase subunit 8 (Fragment).  
 GN Name=ATPase 8;  
 OS Eurypharynx pelecanoides (pelican eel).  
 OC Mitochondrion;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
 OC Eurypharyngidae; Eurypharynx.  
 NCBI\_TaxID=55117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=23967687; PubMed=12294914;  
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";  
 RT Mol. Biol. Evol. 20:1917-1924 (2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
 RT Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB046487; BAB87160; 1; -.  
 DR GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match Similarity 27.4%; Score 23; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 6.2e+03; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative

Qy	4 MDPPP 8	:   :	Db	4 LDPSp 8
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RESULT 15  
 BAB87160 PRELIMINARY; PRY; 10 AA.  
 ID BAB87160  
 AC BAB87160;  
 DT 02-MAR-2004 (TREMBREL 27, Created)  
 DT 03-MAR-2004 (TREMBREL 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBREL 27, Last annotation update)  
 DR ATPase subunit 8 (Fragment).  
 GN ATTPASE 8.  
 OS Burypopharynx pelecanoides (pelican eel).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
 OC Burypopharyngidae; Burypopharynx.  
 OC NCBI\_TAXID=55117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAINED;  
 RA Inoue J.-G., Miya M., Tsukamoto K., Nishida M.;  
 RT "Evolution of the Deep-Sea Gulper Bel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Bels";  
 RL Mol. Biol. Evol. 20:1917-1924(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAINED;  
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AB046487; BAB87160.1; -.  
 KW Mitochondrion.  
 FT NON-TER 10 10  
 SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;  
 Query Match Similarity 27.4%; Score 23; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 6.2e+03; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative

Qy	4 MDPPP 8	:   :	Db	4 LDPSp 8
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Search completed: January 6, 2005, 11:08:29  
 Job time : 190 secs

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## OM protein - protein search, using sw model

Run on: January 6, 2005, 10:51:24 ; Search time 149 seconds

(without alignments) ; 36.114 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKANDPTPPFLWIKR 15

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0  
Maximum DB seq length: 15Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04;\*

- 1: geneseqD19808;\*
- 2: geneseqD19908;\*
- 3: geneseqD20008;\*
- 4: geneseqD20018;\*
- 5: geneseqD20028;\*
- 6: geneseqD20038;\*
- 7: geneseqD20039;\*
- 8: geneseqD20048;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT	1
1	84	100.0	15	2 AAW11575	AAW11575	
2	84	100.0	15	2 AAW53841	AAW11575 standard; peptide; 15 AA.	
3	84	100.0	15	7 ABB80223	XX	
4	69	82.1	12	7 ABB80225	AC	AAW11575;
5	65	77.4	11	7 ABB80226	XX	
6	54	64.3	10	5 AAW53843	XX	
7	54	64.3	10	7 ABB80222	PR	25-MAR-2003 (revised)
8	50	59.5	9	7 ABB80227	XX	20-MAR-1997 (first entry)
9	43	51.2	8	7 ABB80228	PA	
10	41	48.8	9	6 ABR12621	PA	
11	41	48.8	9	6 ABR12017	PI	N-terminal peptide from lethal toxin neutralising factor.
12	41	48.8	9	5 ABR12854	XX	Lethal toxin neutralising factor; LTNF; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
13	41	48.8	10	6 ABR12743	XX	Didelphis virginiana.
14	41	48.8	10	6 ABR11875	XX	US5576597-A.
15	41	48.8	10	6 ABR12121	XX	19-NOV-1996.
16	41	48.8	10	6 ABR12948	XX	PD
17	41	48.8	10	6 ABR1106	XX	22-SEP-1994; 94US-00058387.
18	41	48.8	10	6 ABR12294	XX	10-MAY-1993; 93US-00058387.
19	41	48.8	10	6 ABR12738	XX	PT
20	41	48.8	15	6 ABR3125	XX	Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal peptide.
21	41	48.8	15	6 ABR3383	XX	PT
22	41	48.8	15	6 ABR3116	XX	PT
23	41	48.8	15	6 ABR3427	XX	PT
24	41	48.8	15	6 ABR3363	CC	Claim 7; Col 9; 9pp; English.
25	45.2	48.8	9	2 AAW21252	CC	The present sequence is from the N-Terminal of a 68 kD protein purified from the serum of the opossum Didelphis virginiana. The full-length protein is a lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N-terminal Peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTNF and the 15mer peptide against venom from snakes of the families Crotalidae, Elapidae, Hydrophiidae and Viperidae. (Updated on 25-MAR-2003 to correct PP field.)

SQ	Sequence 15 AA:	100.0%; Score 84; DB 2; Length 15;	ABB80223	RESULT 3
	Query Match	Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ID ABB80223	standard; peptide; 15 AA.
QY	1	LKAMDPTPPWIKTE 15	XX	
DB	1	LKAMDPTPPWIKTE 15	AC ABB80223;	
			XX	
	RESULT 2		DT 06-NOV-2003	(first entry)
	AAW53841		DR Synthetic LTNF, LT-15.	
	ID AAW53841	standard; peptide; 15 AA.	XX	
	KW AAW53841;		XX	
	AC		XX	
	XX		XX	Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGE; nerve growth factor; NCF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
	DT 08-JUL-1998	(first entry)	XX	
	XX		OS Synthetic.	
	DB	N-terminus of opossum LTNF.	XX	
	XX		PN WO2003060471-A2.	
	KW		XX	
	LTNF; Lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.		PD 24-JUL-2003.	
	KW		XX	
	XX		PR 14-JAN-2003; 2003WO-US001044.	
	OS		XX	
	bidelphis virginiana.		PR 14-JAN-2002; 2002US-00047945.	
	XX		XX	
	PN	US5744449-A.	PA (LIPPS/) LIPPS B V.	
	XX		PA (LIPPS/) LIPPS F W.	
	PP	28-APR-1998.	XX	
	XX		PI Lipps BV, LIPPS FW;	
	PP	03-JUN-1996;	XX	
	XX	96US-00657163.	DR WPI; 2003-636703/60.	
	PR		XX	
	XX	10-MAY-1993;	XX	
	PR	93US-00058387.	XX	
	XX	22-SEP-1994;	XX	
	PA	94US-00310340.	XX	
	(LIPPS/)	LIPPS B V.	XX	
	PA	(LIPPS/)	PA (LIPPS/) LIPPS F W.	
	XX		XX	
	PI	LIPPS FW, LIPPS BV;	PI Lipps BV, LIPPS FW;	
	XX		XX	
	DR	WPI; 1998-271108/24.	XX	
	XX		XX	
	PT	Lethal Toxin Neutralising Factor Peptide from opossum - can neutralise venom(s) from all major families of poisonous snakes.	CC	
	PT		CC	
	XX		CC	
	PT	Claim 1; Col 11; 1LIP; English.	CC	
	XX		CC	
	CC	This sequence represents the peptide of the invention. It is a lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity to horse proteins	CC	
	XX		CC	
	CC		CC	
	CC	The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF). Peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythema nodosum (EN), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Grave's disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA.	CC	
	XX		CC	
	SQ	Sequence 15 AA:	XX	
	Query Match	100.0%; Score 84; DB 7; Length 15;	Query Match	100.0%; Score 84; DB 7; Length 15;
	Best Local Similarity	100.0%; Pred. No. 2e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity	100.0%; Pred. No. 2e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	1LKAMDPTPPWIKTE 15	QY 1	1LKAMDPTPPWIKTE 15
DB	1	1LKAMDPTPPWIKTE 15	DB 1	1LKAMDPTPPWIKTE 15
				RESULT 4
				ABB80225

XX	ID	ABB80225	Standard; peptide; 12 AA.	XX	DT	06-NOV-2003 (first entry)
AC				XX	DR	Synthetic LTNF, LT-11.
XX	DT	06-NOV-2003 (first entry)	XX	DR	Synthetic LTNF, LT-11.	
DT	06-NOV-2003 (first entry)	XX	Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjögren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.			
Synthetic.	XX	KW	IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjögren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.			
OS	XX	KW	Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.			
Synthetic.	XX	KW	IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjögren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.			
PN	XX	KW	Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.			
WO2003060471-A2.	XX	OS	Synthetic.			
PD	XX	XX	WO2003060471-A2.			
24-JUL-2003.	XX	XX	24-JUL-2003.			
14-JAN-2003; 2003WO-US001044.	XX	XX	14-JAN-2003; 2003WO-US001044.			
PR	XX	XX	14-JAN-2003; 2003WO-US001044.			
14-JAN-2002; 2002US-00047945.	XX	XX	14-JAN-2002; 2002US-00047945.			
PA	XX	XX	PA (LIPP/) LIPPS B V.			
(LIPP/)	XX	XX	PA (LIPP/) LIPPS F W.			
PA (LIPP/)	XX	XX	PA (LIPP/) LIPPS F W.			
Lipps BV, Lipps FW;	XX	XX	Lipps BV, Lipps FW;			
PI	XX	XX	DR			
Lipps BV, Lipps FW;	XX	XX	WPI; 2003-636703/60.			
PT	XX	XX	PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.			
PT	XX	XX	PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.			
PT	XX	XX	PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.			
PT	XX	XX	PS Claim 7; Page 4; 24pp; English.			
PS	XX	XX	CC The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjögren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA.			
PS	XX	XX	CC The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjögren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA.			
Sequence 12 AA;	XX	XX	SQ Sequence 11 AA;			
Query Match	82.1%	Score	69;	DB	7;	Length 12;
Best Local Similarity	100.0%	Pred. No.	0.00038;	Matches	11;	Conservative 0;
Matchees	12;	Mismatches	0;	Indels	0;	Gaps 0;
QY	1	1	LKAMDPPTPPWI	12	Db	1 LKAMDPPTPW 11
Db	1	1	LKAMDPPTPW	12	Db	1 LKAMDPPTPW 11
RESULT 5	XX	XX	RESULT 6	XX	XX	XX
ABB80226	ID	ABB80226 standard; peptide; 11 AA.	AAM53843	ID	AAM53843	ID
ABB80226	AC		AAM53843	AC	AAM53843	AC
ABB80226;	XX		08-JUL-1998 (first entry)	XX		XX

DB N-terminus of opossum LTNF.  
 XX  
 KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;  
 KW anti-haemorrhagic protein; Blapidae; Viperidae; sea snake; snake bite;  
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;  
 KW histamine reaction treatment.  
 XX Didelphis virginiana.  
 OS US5744449-A.  
 XX PD 28-APR-1998.  
 XX PP 03-JUN-1996; 96US-00657163.  
 XX PR 10-MAY-1993; 93US-00058387.  
 XX PR 22-SEP-1994; 94US-00310340.  
 PA (LIPPS/) LIPPS B V.  
 PA (LIPPS/) LIPPS F W.  
 XX PI Lipps FW, Lipps BV;  
 DR WPI: 1998-271108/24.  
 PT Lethal Toxin Neutralising Factor Peptide from opossum - can neutralise  
 PT venom(s) from all major families of poisonous snakes.  
 XX Claim 7; Col 11; 1LPP; English.

This sequence represents the peptide of the invention. It is a lethal  
 CC toxin neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic  
 CC protein derived from an opossum. The peptide can be used in a method for  
 CC treating a victim of envenomation from a poisonous snake, preferably a  
 CC poisonous snake from the family of Blapidae, Viperidae or sea snake. It  
 CC is useful for the treatment of snake bites, sepsis, allergies caused by  
 CC the environment and treatment of bee or scorpion stings or toxicities  
 CC caused by plant or bacterial toxins. The peptide can also be used in  
 CC histamine reaction treatment. The peptide can be used in envenomation  
 CC treatment for a variety of snakes without prior identification of the  
 CC snake. Being short it can be synthetically prepared rather than the  
 CC current production in horses, where some people can show hypersensitivity  
 CC to horse proteins

XX Sequence 10 AA:  
 SQ Query Match 64.3%; Score 54; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.074; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY QY 1 LKAMDPTPPL 10  
 Db 1 LKAMDPTPPL 10

RESULT 7  
 ABB80222 ID ABB80222 standard; peptide; 10 AA.  
 XX AC ABB80222;  
 XX DT 06-NOV-2003 (first entry)

RESULT 8  
 ID ABB80227  
 XX ABB80227 standard; peptide; 9 AA.  
 XX AC ABB80227;  
 XX DT 06-NOV-2003 (first entry)  
 XX DB Synthetic LTNF, LT-9.

XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;  
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;  
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;  
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;  
 KW IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;  
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;  
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;  
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;  
 KW saliva; ELISA.  
 OS Synthetic.

XX OS Synthetic.

XX PN WO2003060471-A2.  
 XX PD 24-JUL-2003.  
 XX PR 14-JAN-2003; 2003WO-US001044.  
 XX PR 14-JAN-2002; 2002US-00047945.  
 XX PR (LIPPS/) LIPPS B V.  
 PA (LIPPS/) LIPPS F W.  
 XX PI Lipps BV, Lipps FW;  
 DR WPI: 2003-636703/60.  
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

XX PS Claim 7; Page 3; 24PP; English.

XX CC The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) Peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA.

XX SQ Sequence 10 AA:  
 SQ Query Match 64.3%; Score 54; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.074; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY QY 1 LKAMDPTPPL 10  
 Db 1 LKAMDPTPPL 10

RESULT 9  
 ID ABB80227  
 XX ABB80227 standard; peptide; 9 AA.  
 XX AC ABB80227;  
 XX DT 06-NOV-2003 (first entry)

XX DB Synthetic LTNF, LT-9.

XX Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;  
 KW IGE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;  
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;  
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;  
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;  
 KW saliva; ELISA.  
 OS Synthetic.

XX OS Synthetic.

XX PN WO2003060471-A2.

PD XX  
 XX PR XX 14-JAN-2003; 2003WO-US001044.  
 PP XX  
 XX PA (LIPPS/) LIPPS B V.  
 PR XX  
 XX PA (LIPPS/) LIPPS P W.  
 XX PI  
 XX LIPPS BV, Lipps FW;  
 XX DR  
 XX DR WPI; 2003-636703/60.  
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

PS Claim 7; Page 4; 24pp; English.

CC The sequences given in ABB0222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin G (IgG), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgG levels e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA

XX Sequence 9 AA;

Query Match 59.5%; Score 50; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ||||| | | |  
 Db 1 LKAMDPTPP 9

RESULT 9

ID ABB0228  
 ID ABB0228 standard; peptide; 8 AA.

XX AC  
 XX AC ABB0228;  
 XX DT 06-NOV-2003 (first entry)

DB Synthetic LTNF, LT-8.

XX KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's Syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.

XX OS Synthetic.

XX Synthetec.

XX WO2003060471-A2.

XX 24-JUL-2003.

PD XX  
 XX PR 10-APR-2001; 2001US-0282779P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSYS INC.

PS Claim 7; Page 4; 24pp; English.

CC The sequences given in ABB0222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin G (IgG), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgG levels e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA

XX Sequence 8 AA;

Query Match 51.2%; Score 43; DB 7; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8  
 Db 1 LKAMDPTPP 8

RESULT 10

ID ABR12621  
 ID ABR12621 standard; peptide; 9 AA.

XX AC ABR12621;

XX DT 19-MAY-2003 (first entry)

XX KW Human cancer-related protein 156P1D4 HLA peptide #856.

XX KW Human; cytotoxic; vaccine; cancer; immune response; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PR 10-APR-2002; 2002WO-US0011654.

XX PR 10-APR-2001; 2001US-0282779P.

XX PR 10-APR-2001; 2001US-0283112P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSYS INC.

PS Claim 7; Page 4; 24pp; English.

CC The sequences given in ABB0222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin G (IgG), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgG levels e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA

XX Sequence 8 AA;

Query Match 51.2%; Score 43; DB 7; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTP 8  
 Db 1 LKAMDPTPP 8

RESULT 10

ID ABR12621  
 ID ABR12621 standard; peptide; 9 AA.

XX AC ABR12621;

XX DT 19-MAY-2003 (first entry)

XX KW Human cancer-related protein 156P1D4 HLA peptide #856.

XX KW Human; cytotoxic; vaccine; cancer; immune response; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PR 10-APR-2002; 2002WO-US0011654.

XX PR 10-APR-2001; 2001US-0282779P.

XX PR 10-APR-2001; 2001US-0283112P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSYS INC.

PI	Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;	PS	Claim 13, Page 232; 1021pp; English.
XX	Morrison K, Morrison RK, Raitano AB;	CC	The present invention relates to novel human cancer-related genes and proteins (ABZ7120-ABZ78168 and ABR01789-ABR01861). The gene and proteins are useful for eliciting a humoral or cellular immune response.
DR	WPI; 2003-075555/07.	CC	The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
XX	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.	CC	CC
PT	Claim 13; Page 238; 1021pp; English.	CC	CC
PT	The present invention relates to novel human cancer-related genes and proteins (ABZ7120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention	CC	CC
PS	Sequence 9 AA;	CC	CC
XX	Query Match 48.8%; Score 41; DB 6; Length 9; Best Local Similarity 66.7%; Pred. No. 1.7e+06; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	SQ	Query Match 48.8%; Score 41; DB 6; Length 9; Best Local Similarity 66.7%; Pred. No. 1.7e+06; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db	QY 4 MDPTPPW1 12     :     1 MDPSVPIWI 9	DB	QY 4 MDPTPPW1 12     :     1 MDPSVPIWI 9
RESULT 11	ABR12017 standard; peptide; 9 AA.	RESULT 12	ABR12054
ID	ABR12017;	ID	ABR12054 standard; peptide; 9 AA.
AC	ABR12017;	XX	ABR12054;
DB	19-MAY-2003 (first entry)	DT	19-MAY-2003 (first entry)
XX	DR Human cancer-related protein 156P1D4 HLA peptide #1089.	XX	DR Human cancer-related protein 156P1D4 HLA peptide #1089.
XX	KW Human; cytostatic; vaccine; cancer; immune response; HLA;	XX	KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX	KW human leukocyte antigen.	OS	KW human leukocyte antigen.
OS	Homo sapiens.	OS	Homo sapiens.
XX	WO200283921-A2.	PN	WO200283921-A2.
XX	PD 24-OCT-2002.	XX	PD 24-OCT-2002.
PP	10-APR-2002; 2002WO-US011654.	PP	10-APR-2002; 2002WO-US011654.
XX	PR 10-APR-2001; 2001US-0282739P.	XX	PR 10-APR-2001; 2001US-0282739P.
PR	PR 10-APR-2001; 2001US-0283112P.	PR	PR 10-APR-2001; 2001US-0283112P.
DR	DR 25-APR-2001; 2001US-0286630P.	DR	DR 25-APR-2001; 2001US-0286630P.
XX	PA (AGEN-) AGENSYN INC.	XX	PA (AGEN-) AGENSYN INC.
XX	PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;	XX	PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;
PI	PI Morrison K, Morrison RK, Raitano AB;	XX	PI Morrison K, Morrison RK, Raitano AB;
XX	WPI; 2003-075555/07.	DR	WPI; 2003-075555/07.
XX	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.	PT	The present invention relates to novel human cancer-related genes and proteins (ABZ7120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention
XX	Claim 13; Page 240; 1021pp; English.	CC	CC
XX	Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;	CC	CC
PI	Morrison K, Morrison RK, Raitano AB;	CC	CC
XX	WPI; 2003-075555/07.	CC	CC
XX	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.	CC	CC
PT	The present invention relates to novel human cancer-related genes and proteins (ABZ7120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention	CC	CC
PT	Claim 13; Page 240; 1021pp; English.	CC	CC
PT	Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;	CC	CC
PT	Morrison K, Morrison RK, Raitano AB;	CC	CC
XX	WPI; 2003-075555/07.	CC	CC
XX	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.	CC	CC

Page 7

CC as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

	Best Local Similarity	Pred.	No.	Indels	Gaps
Matches	65.7%	1.7e+06	1	0	0
QY	6; Conservative	2; Mismatches	1	0	0
DB	4 MDPTPPIWI 1     :   :   1 MDPSVPIWI	12 9			

ID ABR1:875 standard; peptide; 10 AA.  
XX  
AC ABR1:875;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DB Human cancer-related protein 156P1D4 HLA peptide #110.  
KW Human; cytostatic; vaccine; cancer; immune response; HLA peptide; 10 AA.

ID ABR12743 Standard; peptide; 10 AA.  
 XX  
 AC  
 XX  
 DT 19-MAY-2003 (First entry)  
 XX  
 DE Human cancer-related protein 156P16 HLA peptide #978.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.

PN WO200283921-A2.  
XX  
XX  
PD 24-OCT-2002.  
XX  
PP 10-APR-2002; 2002WO-US011654.  
XX

PR 10-APR-2001; 2001US-0282739P.  
PR 10-APR-2001; 2001US-0283112P.  
PR 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSY INC.

Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS; PI Morrison K, Morrison RK, Raitano AB; DR WPI; 2003-075555/07.

PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT man and animal.

Claim 13; Page 239; 1021pp; English.

Claim 13: Page 231; 1021pp; English.

The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagent for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC  
XX  
SQ

Query Match      48.8%; Score 41; DB 6; Length 10;  
 Best Local Similarity      66.7%; Pred. No. 8.5; Mismatches 2;  
 Matches 6; Conservative 2; Mismatches 1; Indexes 0; Gaps 0

AC ABR12121;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DB Human cancer-related protein 156P1D4 HLA peptide #356.  
 XX  
 KW Human; Cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PR 10-APR-2002; 2002WO-US011654.  
 XX  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSYN INC.  
 XX  
 PI Jakobovits A, Chaillita-Bid PM, Paris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 DR XX  
 WPI: 2003-075555/07.

XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 XX cancer patients.

RS Claim 13; Page 233; 1021pp; English.

XX  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (AB278120-AB278168 and AB01789-AB01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 The genes are useful as probes and primers for the amplification and/or  
 detection of genes, mRNAs or their fragments, as reagents for the  
 diagnosis and/or prognosis of cancer, as coding sequences capable of  
 directing the expression of the protein, as tools for modulating or  
 inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention

SQ Sequence 10 AA;

Query	Match	Similarity	Score	DB	Length
Best Local Matches	6	66.7%	41	6	10
Conservative	2				
Mismatches	1				
Indels	0				
Gaps	0				

QY 4 MDPPPLWI 12  
 Db 1 MDPSVPIWI 9

Search completed: January 6, 2005, 11:05:15  
 Job time : 151. secs

GenCore version 5.1.6  
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## Om protein - protein search, using sw model

Run on: January 6, 2005, 11:08:35 ; Search time 141 Seconds

(without alignments)  
 38.359 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPTPPLWIKTB 15

Scoring table: BL0SUM62

Gapop 10.0 , Gapext: 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 251122

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*

1: /cgn2\_6/ptodata/1/pubbaa/US07\_PUBCOMB.pep: \*

2: /cgn2\_6/ptodata/1/pubbaa/PCT\_NEW\_PUB.pep: \*

3: /cgn2\_6/ptodata/1/pubbaa/US06\_PUBCOMB.pep: \*

4: /cgn2\_6/ptodata/1/pubbaa/US06\_PUBCOMB.pep: \*

5: /cgn2\_6/ptodata/1/pubbaa/US07\_NEW\_PUB.pep: \*

6: /cgn2\_6/ptodata/1/pubbaa/ACTUS\_PUBCOMB.pep: \*

7: /cgn2\_6/ptodata/1/pubbaa/US08\_PUBCOMB.pep: \*

8: /cgn2\_6/ptodata/1/pubbaa/PCT\_NEW\_PUB.pep: \*

9: /cgn2\_6/ptodata/1/pubbaa/US09\_PUBCOMB.pep: \*

10: /cgn2\_6/ptodata/1/pubbaa/US09C\_PUBCOMB.pep: \*

11: /cgn2\_6/ptodata/1/pubbaa/US10\_PUBCOMB.pep: \*

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13: /cgn2\_6/ptodata/1/pubbaa/US10B\_PUBCOMB.pep: \*

14: /cgn2\_6/ptodata/1/pubbaa/US10C\_PUBCOMB.pep: \*

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16: /cgn2\_6/ptodata/1/pubbaa/US10\_EU\_PUBCOMB.pep: \*

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18: /cgn2\_6/ptodata/1/pubbaa/US11\_NEW\_PUB.pep: \*

19: /cgn2\_6/ptodata/1/pubbaa/US60\_PUBCOMB.pep: \*

20: /cgn2\_6/ptodata/1/pubbaa/US60\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	84	100.0	15	14	US-10-047-945-2
2	69	82.1	12	14	US-10-047-945-4
3	65	77.4	11	14	US-10-047-945-5
4	54	64.3	10	14	US-10-047-945-1
5	50	59.5	9	14	US-10-047-945-6
6	43	51.2	8	14	US-10-047-945-7
7	37	44.0	15	14	US-10-161-791-44
8	34	40.5	12	14	US-10-286-457-239
9	34	40.5	12	16	US-10-327-597-735
10	33	39.3	9	15	US-10-157-475B-10923
11	33	39.3	9	15	US-10-154-884B-10923
12	33	39.3	13	15	US-10-468-370-501
13	33	39.3	13	15	US-10-468-370-502

and is derived by analysis of the total score distribution.

## ALIGNMENTS

## RESULT 1

; Sequence 2, Application US/10047945

; Publication No. US2003015755A1

; GENERAL INFORMATION:

; APPLICANT: LIPPS, BRIAN V.

; APPLICANT: LIPPS, FREDERICK W.

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E

; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS

; FILE REFERENCE: WIPIAT015US

; CURRENT APPLICATION NUMBER: US/10/047-945

; CURRENT FILING DATE: 2002-01-14

; PRIOR APPLICATION NUMBER:

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS

; SEQ ID NO: 2

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: NAME/KEY:

; LOCATION:

; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM

; OTHER INFORMATION: US 5,576,297.

; US-10-047-945-2

Query Match 100.0%; Score 84; DB 14; Length 15;  
 Best local similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 15; Conservative 1 LKAMDPTPPLWIKTB 15  
 QY 1 LKAMDPTPPLWIKTB 15  
 Db 1 LKAMDPTPPLWIKTB 15

RESULT 2  
US-10-047-945-4

; Sequence 4, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINTE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS  
; FILE REFERENCE: FWLPA101US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.

US-10-047-945-4

Query Match 82.1%; Score 69; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;

Qy	Db										
1	1	LKAMDPPTPPLW	I	12							

RESULT 3  
US-10-047-945-5

; Sequence 5, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINTE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS  
; FILE REFERENCE: FWLPA101US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.

US-10-047-945-5

Query Match 82.1%; Score 69; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;

Qy	Db										
1	1	LKAMDPPTPPLW	I	12							

RESULT 4  
US-10-047-945-1

; Sequence 1, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINTE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS  
; FILE REFERENCE: FWLPA101US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.

US-10-047-945-1

Query Match 82.1%; Score 69; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0017; Mismatches 0; Indels 0; Gaps 0;

Qy	Db										
1	1	LKAMDPPTPPLW	I	12							

RESULT 5  
US-10-047-945-6

; Sequence 6, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINTE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS  
; FILE REFERENCE: FWLPA101US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.

US-10-047-945-6

Query Match 59.5%; Score 50; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;

Qy	Db									
1	1	LKAMDPPTP	I	9						

RESULT 6  
US-10-047-945-7

; Sequence 7, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:

```

; APPLICANT: LIPPS, BINIE V.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; FILE REFERENCE: FWPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; PRIORITY FILING DATE: 2002-01-14
; PRIORITY APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORPPERFECT 5.1 FOR WINDOWS
; SEQ ID NO: 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
US-10-047-945-7

Query Match      51.2%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 8 ; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 LKAMDPTP 8
Db   1 LKAMDPTP 8

RESULT 7
US-10-161-791-444

Sequence 444, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OULLIUM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penne & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEX: 66141 PENNE
; INFORMATION FOR SEQ ID NO: 444:

Query Match      44.0%; Score 37; DB 14; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6 ; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy   2 KAMDPTPL 10
Db   5 RALPPTPL 13

RESULT 8
US-10-286-457-239

Sequence 239, Application US/10286457
Publication No. US20030166094A1
GENERAL INFORMATION:
APPLICANT: JENO GYURIS ET AL.
TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
FILE REFERENCE: GCP1-P01-178
CURRENT APPLICATION NUMBER: US/10/286,457
PRIORITY FILING DATE: 2002-11-01
PRIORITY APPLICATION NUMBER: 60/334822
NUMBER OF SEQ ID NOS: 684
SOFTWARE: Patentin version 3.1
SEQ ID NO: 239
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence isolated from random peptide libraries, base
OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-239

Query Match      40.5%; Score 34; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4 ; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy   8 PRPWIKTE 15
Db   3 PPTWLQTQ 10

RESULT 9
US-10-327-598-735

Sequence 735, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Alayappa, Ashok
APPLICANT: Lawton, Robert
APPLICANT: Ayappa, Ashok
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
TITLE OF INVENTION: For Making and Using Them
FILE REFERENCE: 01-799A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIORITY APPLICATION NUMBER: US 60/344,874
PRIORITY FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: Patentin version 3.0
SEQ ID NO: 735
LENGTH: 12
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-735

Query Match      40.5%; Score 34; DB 16; Length 12;

```

Best Local Similarity 62.5%; Pred. No. 2.5e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAMDTPP 9

Db 1 QSFPTPP 8

---

RESULT 10

US-10-057-475B-10923

; Sequence 10923, Application US/10057475B

; Publication No. US201004000568A1

; GENERAL INFORMATION:

; APPLICANT: Galger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Clapper, Jonathan David

; APPLICANT: Wang, Ajun

; APPLICANT: Ordonez, Nadia

; APPLICANT: Carter, Lauren

; APPLICANT: McNeill, Patricia Dianne

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of Hematological Malignancies

; FILE REFERENCE: 014058-014402US

; CURRENT APPLICATION NUMBER: US10/154,884B

; CURRENT FILING DATE: 2002-05-23

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-03-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 10923

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide

; US-10-154-884B-10923

Query Match Best Local Similarity 39.3%; Score 33; DB 15; Length 9;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPLWIKT 14

Db 3 PPLWIKT 9

---

RESULT 12

US-10-468-370-501

; Sequence 501, Application US/10468370

; Publication No. US20040082039A1

; GENERAL INFORMATION:

; APPLICANT: Gillies, Stephen

; APPLICANT: Carr, Francis J.

; APPLICANT: Jones, Tim

; APPLICANT: Carter, Graham

; APPLICANT: Hamilton, Anita

; APPLICANT: Williams, Stephen

; APPLICANT: Hanlon, Marian

; APPLICANT: Watkins, John

; APPLICANT: Baker, Matthew

; APPLICANT: Way, Jeffrey

; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED IMMUNOGENICITY

; FILE REFERENCE: MER-118

; CURRENT APPLICATION NUMBER: US/10/0468,370

; CURRENT FILING DATE: 2003-08-19

; PRIOR APPLICATION NUMBER: EP 01103955.9

; PRIOR FILING DATE: 2001-02-19

; PRIOR APPLICATION NUMBER: EP 01108291.4

; PRIOR FILING DATE: 2001-04-05

RESULT 11

US-10-154-884B-10923

; Sequence 10923, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

PRIOR APPLICATION NUMBER: PCT/EP02/01690  
; NUMBER OF SEQ ID NOS: 699  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 501  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MHC class II binding epitope  
; US-10-468-370-501

Query Match Best Local Similarity 62.5%; Pred. No. 3.8e+02; Length 13; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TPPLWIKT 14  
Db 4 TSPTWIKT 11

RESULT 13  
US-10-468-370-502  
; Sequence 502, Application US/10468370  
; Publication No. US20040082059A1  
GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Carr, Francis J.  
; APPLICANT: Jones, Tim  
; APPLICANT: Carter, Graham  
; APPLICANT: Hamilton, Anita  
; APPLICANT: Williams, Stephen  
; APPLICANT: Hanlon, Marian  
; APPLICANT: Watkins, John  
; APPLICANT: Baker, Matthew  
; APPLICANT: Way, Jeffrey  
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED LENGTH: 13  
FILE REFERENCE: MER-118  
CURRENT APPLICATION NUMBER: US/10/468,370  
CURRENT FILING DATE: 2003-08-19  
PRIORITY NUMBER: EP 01103955.9  
PRIOR APPLICATION NUMBER: EP 01103951.4  
PRIOR FILING DATE: 2001-04-05  
PRIORITY NUMBER: PCT/EP02/01690  
PRIORITY FILING DATE: 2002-02-18  
NUMBER OF SEQ ID NOS: 689  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 502  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: MHC class II binding epitope  
; US-10-468-370-502

Query Match Best Local Similarity 62.5%; Pred. No. 3.8e+02; Length 13; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TPPLWIKT 14  
Db 4 TSPTWIKT 11

RESULT 14  
US-10-468-370-502  
; Sequence 502, Application US/10468370  
; Publication No. US20040082059A1  
GENERAL INFORMATION:  
; APPLICANT: Carr, Francis J.  
; APPLICANT: Carter, Graham  
; APPLICANT: Hamilton, Anita  
; APPLICANT: Williams, Stephen  
; APPLICANT: Jones, Tim  
; APPLICANT: Baker, Matthew  
; APPLICANT: Way, Jeffrey  
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED LENGTH: 13  
FILE REFERENCE: MER-118  
CURRENT APPLICATION NUMBER: US/10/468,370  
CURRENT FILING DATE: 2003-08-19  
PRIORITY NUMBER: EP 01103955.9  
PRIOR APPLICATION NUMBER: EP 01103951.4  
PRIOR FILING DATE: 2001-04-05  
PRIORITY NUMBER: PCT/EP02/01690  
PRIORITY FILING DATE: 2002-02-18  
NUMBER OF SEQ ID NOS: 689  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 502  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: MHC class II binding epitope  
; US-10-468-370-502

Query Match Best Local Similarity 62.5%; Score 33; DB 15; Length 13; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TPPLWIKT 14  
Db 1 TSPTWIKT 8

RESULT 15  
US-10-468-496-458  
; Sequence 458, Application US/10468496  
; Publication No. US2004180386A1  
GENERAL INFORMATION:  
; APPLICANT: Carr, Francis J.  
; APPLICANT: Carter, Graham  
; APPLICANT: Jones, Tim  
; APPLICANT: Hamilton, Anita  
; APPLICANT: Williams, Stephen  
; APPLICANT: Baker, Matthew  
; APPLICANT: Way, Jeffrey  
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL LENGTH: 13  
FILE REFERENCE: MER-117  
CURRENT APPLICATION NUMBER: US/10/468,496  
CURRENT FILING DATE: 2003-09-25  
PRIORITY NUMBER: 01103954.2  
PRIOR FILING DATE: 2001-02-19  
PRIORITY NUMBER: 01105777.5  
PRIOR FILING DATE: 2001-03-08  
PRIORITY NUMBER: 0110538.0  
PRIOR FILING DATE: 2001-03-15  
PRIORITY NUMBER: 0110536.4  
PRIOR FILING DATE: 2001-03-15  
PRIORITY NUMBER: 01107012.5  
PRIOR FILING DATE: 2001-03-20  
PRIORITY NUMBER: 0110689.6  
PRIOR FILING DATE: 2001-03-20  
PRIORITY NUMBER: 0110689.6  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 458  
LENGTH: 13  
TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MHC class II binding epitope  
US-10-468-456-458

Query Match 39.3%; Score 33; DB 16; Length 13;  
Best Local Similarity 62.5%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 7 TPPWIKT 14  
| : |  
Db 1 TSPWIKT 8

Search completed: January 6, 2005, 11:20:33  
Job time : 142 secs

GenCore version 5.1.6  
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On protein - protein search, using SW model

Run on: January 6, 2005, 11:02:50 ; Search time 37 Seconds  
 (without alignments)  
 26.886 Million cell updates/sec

Title: US-10-047-945-2  
 Perfect score: 64  
 Sequence: 1 LKAMDPPTPLWIKTB 15

Scoring table: BIOSUM62  
 Gapext 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0  
 Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AW:  
 1: /cgtn2\_6/ptodata/1/iaa/5A\_COMB.pep: \*  
 2: /cgtn2\_6/ptodata/1/iaa/5B\_COMB.pep: \*  
 3: /cgtn2\_5/ptodata/1/iaa/5A\_COMB.pep: \*  
 4: /cgtn2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
 5: /cgtn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep: \*  
 6: /cgtn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	84	100.0	15 1	US-05-310-340A-1
2	84	100.0	15 1	US-05-310-340A-1
3	54	64.3	10 1	US-05-657-163A-2
4	37	44.0	15 3	US-05-602-999A-444
5	37	44.0	15 4	US-05-500-124-444
6	32	38.1	11 1	US-05-336-343A-31
7	32	38.1	11 3	US-05-652-877-31
8	32	38.1	11 3	US-05-475-515A-31
9	32	38.1	12 3	US-05-602-999A-252
10	32	38.1	12 4	US-05-500-124-252
11	32	38.1	14 3	US-05-268-992-70
12	32	38.1	14 3	US-05-657-474-70
13	32	38.1	14 4	US-05-845-583A-13
14	32	38.1	14 4	US-05-547-693A-13
15	31	36.9	13 3	US-05-232-446B-11
16	31	36.9	13 4	US-05-119-5107B-24
17	31	36.9	13 4	US-05-899-556A-24
18	31	36.9	13 4	US-05-547-693-24
19	31	36.9	13 4	US-05-547-693-198
20	30	35.7	6 3	US-05-232-446B-24
21	30	35.7	8 4	US-05-547-693-168
22	30	35.7	10 4	US-05-547-693-165
23	30	35.7	12 2	US-05-659-584A-8
24	30	35.7	12 3	US-05-660-531-8
25	30	35.7	12 4	US-05-995-804B-4
26	30	35.7	13 4	US-05-119-5107B-21
27	30	35.7	13 4	US-05-119-5107B-22

## ALIGNMENTS

RESULT 1  
 US-08-310-340A-1  
 ; Sequence 1, Application US/08310340A  
 ; Patent No. 5576297  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 ; TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR  
 ; TITLE OR INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 ; NUMBER OF SOURCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BINIE V. LIPPS  
 ; STREET: 450 MIMOSA DR.  
 ; CITY: BELLAIRE  
 ; STATE: TEXAS  
 ; COUNTRY: USA  
 ; ZIP: 77401  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB  
 ; COMPUTER: IBM COMPATIBLE  
 ; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 ; SOFTWARE: MS WORD 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/310,340A  
 ; FILING DATE: 22 SEPTEMBER 1994  
 ; CLASSIFICATION: 514  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/058, 387  
 ; FILING DATE: 10 MAY 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME:  
 ; REGISTRATION NUMBER:  
 ; REFERENCE DOCKET NUMBER:  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 713-723-6845  
 ; TELEFAX: 713-663-7290  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15  
 ; TYPE: AMINO ACID  
 ; STRANDEDNESS: SINGLE  
 ; TOPOLogy: LINEAR  
 ; MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N  
 ; ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:  
 ; ORGANISM: DIDELPHIS VIRGINIANA  
 ; STRAIN: WILD



APPLICATION NUMBER: 08/058,387  
 FILING DATE: 10 MAY 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JOHN R. CASPERSON  
 REGISTRATION NUMBER: 28,198  
 REFERENCE/DOCKET NUMBER: FWL-PAT-US-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713-482-2961  
 TELEX: 713-663-7290  
 TELEFAX:

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 MOLECULAR TYPE: PEPTIDE IN SEQ ID NO: 2  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N  
 ORIGINAL SOURCE: SYNTHETIC  
 US-08-657-163A-2

Query Match 64.3%; Score 54; DB 1; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 0; 0.029; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPL 10  
 Db 1 LKAMDPTPPL 10  
 Query Match 44.0%; Score 37; DB 3; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 17; 1; 0.17; 1; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; MisMatches 1; Indels 0; Gaps 0;  
 US-08-602-99A-444  
 Qy 2 KAMDPTPPL 10  
 Db 5 RALPPTPPL 13

RESULT 5  
 Sequence 444, Application US/09500124  
 ; Sequence 444, Application US/09500124  
 ; GENERAL INFORMATION:  
 ; PATENT NO. 6433920  
 ; APPLICANT: SPARKS, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DBR, Channing J.  
 ; APPLICANT: FOWLER, Dana M.  
 ; APPLICANT: RIDER, James E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; NUMBER OF SEQUENCES: 467  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/500,124

FILING DATE: 16-FEB-1996

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/602,999

FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 869-9030

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 444:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPLOGY: unknown

MOLECULE TYPE: peptide

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/602,999  
 FILING DATE: 16-FEB-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mirock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 1101-202  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 869-9030  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 6641 PENNIE  
 INFORMATION FOR SEQ ID NO: 444:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-09-500-124-444  
 Query Match 44.0%; Score 37; DB 4; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 17; 1; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; MisMatches 1; Indels 0; Gaps 0;  
 Qy 2 KAMDPTPPL 10  
 Db 5 RAUPTPPL 13

RESULT 6  
 US-08-336-343A-31  
 ; Sequence 31, Application US/08336343A  
 ; Patent No. 5677144  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ulrich, Axel  
 ; APPLICANT: Alves, Frauke  
 ; TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Penile & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/336-343A  
 ; FILING DATE: 08-NOV-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A.  
 ; REFERENCE/DOCKET NUMBER: 30,742  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 6641 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; US-08-336-343A-31

Query Match 38.1%; Score 32; DB 1; Length 11;  
 Best Local Similarity 56.7%; Pred. No. 74; Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDTPPL 10  
 Db 3 KMPPRPPL 11

RESULT 7  
 US-08-52-877-31  
 ; Sequence 31, Application US/08652877  
 ; Patent No. 618748  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Åkerblom, Goran  
 ; APPLICANT: Juhlin, Claes  
 ; APPLICANT: Rask, Lars  
 ; APPLICANT: Crumley, Gregg R.  
 ; APPLICANT: Morse, Clarence C.  
 ; APPLICANT: Murray, Edward M.  
 ; APPLICANT: Hjalm, Goran  
 ; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
 ; NUMBER OF SEQUENCES: 84  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Martin Savitzky  
 ; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.  
 ; CITY: Collegeville  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19426-0107  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY disk  
 ; COMPUTER: Compaq PC  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: Word 7.0 (PatentIn)

---

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: Macintosh  
 OPERATING SYSTEM: System 7.5.1  
 SOFTWARE: Word 6.0 (PatentIn)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/652,877  
 FILING DATE: 22-NOV-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/15203  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/487,314  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Savitzky, Martin  
 REGISTRATION NUMBER: 29,699  
 REFERENCE/DOCKET NUMBER: A1355B-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-454-3816  
 TELEFAX: 610-454-3808  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 FRAGMENT TYPE: internal  
 US-08-652-877-31

Query Match 38.1%; Score 32; DB 3; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 74; Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAMDTPPL 10  
 Db 3 KMPPRPPL 11

RESULT 8  
 US-08-476-515A-31  
 ; Sequence 31, Application US/08476515A  
 ; Patent No. 6239270  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Åkerblom, Goran  
 ; APPLICANT: Juhlin, Claes  
 ; APPLICANT: Rask, Lars  
 ; APPLICANT: Crumley, Gregg R.  
 ; APPLICANT: Morse, Clarence C.  
 ; APPLICANT: Murray, Edward M.  
 ; APPLICANT: Hjalm, Goran  
 ; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
 ; NUMBER OF SEQUENCES: 84  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Martin Savitzky  
 ; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.  
 ; CITY: Collegeville  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19426-0107  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY disk  
 ; COMPUTER: Compaq PC  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: Word 7.0 (PatentIn)

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,515A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/344,836  
; FILING DATE: 23-NOV-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/SB94/00483  
; FILING DATE: 24-MAY-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: SB 9301764-8  
; FILING DATE: 24-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A1355D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 869-9741/8864  
; TELEFAX: 66141 PENNIE  
; TELX: 66141-PENNIE  
; INFORMATION FOR SEQ ID NO: 252:  
; SEQENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-602-999A-252  
; TOPOLGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
; US-08-476-515A-31

RESULT 9  
US-08-602-999A-252  
; Sequence 252, Application US/08602999A  
; Patent No. 6194205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; COMPUTER TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 252:  
; SEQENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLGY: unknown  
; MOLECULE TYPE: peptide

US-09-500-124-252  
Query Match 38.1%; Score 32; DB 3; Length 12;  
Best Local Similarity 66.7%; Pred. No. 81; Matches 6; Conservative 66.7%; Pred. No. 81; Mismatches 0; Indels 3; Gaps 0;  
Qy 2 KAMDPPTPL 10  
Db 4 KEMPPRPL 12

RESULT 10  
US-09-500-124-252  
; Sequence 252, Application US/09500124  
; Patent No. 642920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; COMPUTER TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 252:  
; SEQENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLGY: unknown  
; MOLECULE TYPE: peptide

US-09-500-124-252

Query Match 38.1%; Score 32; DB 4; Length 12;  
Best Local Similarity 66.7%; Pred. No. 81; Mismatches 3; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	2	KAMDPTPPL	10
Db	4	KWPWPRPPL	12

RESULT 11  
US-09-268-992-70  
; Sequence 70, Application US/09268992  
; Patent No. 6342351  
; GENERAL INFORMATION:  
; APPLICANT: Freimer, N.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING FILE REFERENCE: 783-138  
; CURRENT APPLICATION NUMBER: US/09/268,992  
; CURRENT FILING DATE: 1999-03-16  
; EARLIER APPLICATION NUMBER: 09/236,134  
; EARLIER FILING DATE: 1998-01-22  
; EARLIER APPLICATION NUMBER: 60/106,056  
; EARLIER FILING DATE: 1998-10-28  
; EARLIER APPLICATION NUMBER: 60/088,312  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 60/078,044  
; EARLIER FILING DATE: 1998-03-16  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 70  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens

Query Match 38.1%; Score 32; DB 3; Length 14;  
Best Local Similarity 80.0%; Pred. No. 95; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	7	TPPLW	11
Db	7	TPPIW	11

RESULT 12  
US-09-657-474-70  
; Sequence 70, Application US/09657474  
; Patent No. 6399762  
; GENERAL INFORMATION:  
; APPLICANT: Chen, H.  
; APPLICANT: Preimer, N.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING FILE REFERENCE: 783-138  
; CURRENT APPLICATION NUMBER: US/09/657,474  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 09/268,992  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: 09/236,134  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 60/106,056  
; PRIOR FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: 60/088,312  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: 60/078,044  
; PRIOR FILING DATE: 1998-03-16  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 70  
; LENGTH: 14  
; TYPE: PRT

Query Match 38.1%; Score 32; DB 3; Length 12;  
Best Local Similarity 66.7%; Pred. No. 81; Mismatches 3; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	2	KAMDPTPPL	10
Db	4	KWPWPRPPL	12

RESULT 13  
US-09-845-583A-13  
; Sequence 13, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Burresson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champiland, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583A  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Mus musculus

Query Match 38.1%; Score 32; DB 4; Length 14;  
Best Local Similarity 50.0%; Pred. No. 95; Mismatches 4; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	3	AMDPDPPLWI	12
Db	2	ANSPDPLWV	11

RESULT 14  
US-09-547-693-160  
; Sequence 160, Application US/09547693  
; Patent No. 6639050  
; GENERAL INFORMATION:  
; APPLICANT: Kieliszewski, Marcia  
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
; FILE REFERENCE: OHU-04089  
; CURRENT APPLICATION NUMBER: US/09/547,693  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 236  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 160  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial/Unknown  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Synthetic  
; NAME/KEY: SITE  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; LOCATION: (7)..(7)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
; NAME/KEY: SITE  
; LOCATION: (9)..(10)  
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

; NAME/KEY: SITE  
; LOCATION: (14)...(14)  
; OTHER INFORMATION: The Proline at this position is a hydroxyproline:  
US-09-547-693-160

Query Match	Best Local Similarity	Score	DB	Length	Pred. No.	Gaps	Matches	Indels
Qy	3 AMDPTPP	38.1%	4	14	95;	0	5;	2;
Db	4 SLDPSP	62.5%						

RESULT 15  
US-09-232-446B-11  
; Sequence 11, Application US/09232446B  
; Patent No. 623647  
; GENERAL INFORMATION:  
; APPLICANT: Voytas, Daniel F.  
; APPLICANT: Gai, Xiaowu  
; TITLE OF INVENTION: Transposable Element Protein that Directs DNA  
; FILE REFERENCE: 2-98  
; CURRENT APPLICATION NUMBER: US/09/232,446B  
; CURRENT FILING DATE: 1999-01-15  
; PRIOR APPLICATION NUMBER: US 60/071,383  
; PRIOR FILING DATE: 1998-01-15  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: mutant peptide  
; OTHER INFORMATION: Sequence  
; OTHER INFORMATION: Description of Artificial Sequence: mutant peptide  
US-09-232-446B-11

Query Match	Best Local Similarity	Score	DB	Length	Pred. No.	Gaps	Matches	Indels
Qy	3 AMDPTPP	36.9%	3	13	1.3e+02;	0	4;	0;
Db	4 SLDPSP	57.1%						

Search completed: January 6, 2005, 11:17:35  
Job time : 37 secs

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GenCore version 5.1.6

Om protein - protein search, using SW model

Run on: January 6, 2005, 11:17:41 ; Search time 38 Seconds  
 (without alignment 38 Seconds)

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0  
 Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR 79;\*

1: pir1;\*  
 2: pir2;\*  
 3: pir3;\*  
 4: pir4;\*

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	27	39.1	7	A61081 tryptophyllin, basic - Rohde's leaf frog
2	27	39.1	10	A36545 tryptophyllin, basic - Rohde's leaf frog
3	24	34.8	2	S21288 lectin - potato (f)
4	23	33.3	7	A58725 virotoxin - destro urease (EC 3.5.1.5 peptide-N4-(N-acetyl lysyl-bradykinin - bradykinin-potenti major protein anti enamelin f - bovin glycine reductase trimerogen A-10 - dystrophin-assoc I-cell receptor be exotoxin A - Strep collagen alpha 2(V T-cell receptor be complement C3b rec metallothionein-A alcohol dehydrogen triacylglycerol li hementin (EC 3.4.- seed protein wb-18 T-cell receptor de hypothetical 1.4K hypothetical 1.4K thyroglobulin - ra tachykinin - Afric hypothetical prote
5	21	30.4	10	C35389
6	21	30.4	2	B59272
7	21	30.4	10	S39030
8	21	30.4	11	XAVIBH
9	20	29.0	5	B60274
10	20	29.0	8	S10783
11	20	29.0	8	A39308
12	20	29.0	12	JTJG0
13	20	29.0	2	B30572
14	19	27.5	9	A60108
15	19	27.5	9	A60108
16	19	27.5	9	S26508
17	19	27.5	10	C30572
18	19	27.5	11	D45900
19	18	26.1	2	A49033
20	18	26.1	8	S71919
21	18	26.1	10	PC2171
22	18	26.1	10	A61007
23	18	26.1	11	C61497
24	18	26.1	12	A49033
25	18	26.1	12	JQ2318
26	18	26.1	12	JQ2318
27	18	26.1	12	I58273
28	18	26.1	12	S07436
29	17	24.6	7	S09652

**ALIGNMENTS**

**RESULT 1**

A61081

C:Species: Phylomedusa rohdei (Rohde's leaf frog)  
 C:Accession: A61081  
 R:Montecuccchi, P.C.; Vincenti, M.; Mazzarini, A.M.; Rusconi, L.; Ersparmer, V.  
 Int. J. Pept. Protein Res. 33, 391-395, 1989  
 A:Title: Isolation, structure determination and synthesis of a novel tryptophan-contain A:Reference number: A61081  
 A:Accession: A61081  
 A:Molecule type: protein  
 A:Residues: 1-7 <MON>  
 C:Comment: The biological activity of this peptide was not determined.  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end; hydroxyproline; skin F7/Modified site: 4-hydroxyproline (Pro) #stasis experimental F7/Modified site: amidated carboxyl end (Pro) #stasis experimental

Query Match Similarity Score DB Length  
 Best local 39.1%; 27; 2; 7;  
 Matches 80.0%; Preg. No. 2; 8e+05;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**RESULT 2**

Qy	8	PPMTI	12
Db	2		6

A36454

C:Species: Aedes aegypti (Yellow fever mosquito)  
 C:Accession: A36454; A61630  
 R:Bobrovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
 FASB J. 4, 3015-3020, 1990  
 A:Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme b  
 A:Reference number: A36454; PMID:90367888; PMID:2394318  
 A:Accession: A36454  
 A:Molecule type: protein  
 A:Residues: 1-10 <B02>  
 A:Cross-references: UNIPROT:P19425  
 R:Bobrovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
 Insect Biochem. Mol. Biol. 23, 703-712, 1993  
 A:Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost  
 A:Reference number: A61630; MUID:93357794; PMID:8553526  
 A:Accession: A61630  
 A:Molecule type: protein  
 A:Residues: 1-10 <B02>  
 A:Note: none of the amino acids is modified  
 C:Function:  
 A:Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut e;

C;Keywords: hormone

Query Match 39.1%; Score 27; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPP 9  
Db 2 DPAPP 6

RESULT 3

S21288  
lectin - potato (fragment)

C;Species: Solanum tuberosum (potato)  
C;Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004

C;Accession: S21288  
R;Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.  
Biochem. J. 283, 813-821, 1992  
A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization  
A;Reference number: S21288; MUID:92272683; PMID:1590771

A;Accession: S21288  
A;Molecule type: protein

A;Residues: 1-8 <HHA>

A;Cross-references: UNIPROT:Q7M1V5

A;Experimental source: var. Ulster Sceptre

C;Function:  
A;Description: may be involved in defence mechanism of the plant

C;Keywords: hydroxyproline; lectin

Query Match 34.8%; Score 24; DB 2; Length 8;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 2;

Qy 3 AMDPTPP 9  
Db 2 ASTPSPP 8

RESULT 4

A58725  
Virotoxin - destroying angel

C;Species: Amanita virosa (destroying angel)  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C;Accession: A58725  
R;Faustich, H.; Buku, A.; Bodenmiller, H.; Wieland, T.

Biochemistry 19, 334-343, 1980  
A;Title: Virotoxins: actein-binding cyclic peptides of Amanita virosa mushrooms.

A;Reference number: A58725; MUID:6893271; PMID:6893271

A;Accession: A58725  
A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <FAU>

C;Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide  
P;1-/7/Cross-link: cyclopeptide (Val-Leu) #status experimental

P;2-/Modified site: D-threonine (Thr) #status experimental

P;3-/Modified site: D-serine (Ser) #status experimental

P;4-/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental

P;6-/Modified site: 2'-methysulfonyltryptophan (Trp) #status experimental

P;7-/Modified site: 4,5-dihydroxyleucine (Leu) #status experimental

Query Match 33.3%; Score 23; DB 4; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 2;

Qy 7 TPPW1 12  
Db 2 TSPAWL 7

C;Species: Morganella morganii revision 31-Aug-1990 #text\_change 09-Jul-2004

C;Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 09-Jul-2004  
C;Accession: C35389  
R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.  
J. Bacteriol. 172, 3073-3080, 1990  
A;Reference number: A35389; MUID:90264298; PMID:2345135

A;Accession: C35389  
A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <HHA>

A;Cross-references: UNIPROT:P117339  
C;Keywords: hydrolase

Query Match 30.4%; Score 21; DB 2; Length 10;  
Best Local Similarity 55.7%; Pred. No. 1.2e+03; Indels 0; Gaps 0;

C;Accession: S21288  
C;Species: Prunus dulcis var. sativa (sweet almond)  
C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 09-Jul-2004

C;Accession: B59272  
R;Altmann, P.; Paschinger, K.; Dalik, T.; Vorauer, K.

Eur. J. Biochem. 252, 118-123, 1998  
A;Title: Characterization of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A

A;Reference number: A59272; MUID:98181894; PMID:9523720

A;Accession: B59272  
A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ALT>

A;Cross-references: UNIPROT:P881898  
C;Keywords: hydrolase

Query Match 30.4%; Score 21; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;

C;Accession: S39030  
R;Conlon, J.M.; Olson, K.R.  
FEBS Lett. 334, 75-78, 1993  
A;Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pla

A;Reference number: S39030; MUID:94039817; PMID:8224232

A;Accession: S39030  
A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <CON>

A;Cross-references: UNIPROT:Q9PRZ1

Query Match 30.4%; Score 21; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;

C;Accession: C35389  
C;Species: Morganella morganii (fragment)

RESULT 5  
C35389

## RESULT 8

XAVIBH  
bradykinin-potentiating peptide - halys viper

N;Alternate name: BPP  
C;Species: Agkistrodon halys (halys viper)

C;Accession: JC0002 #sequence\_revision 30-Sep-1988 #text\_change 09-Jul-2004

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 33:9-342, 1985  
A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Molecule type: protein

A;Residues: 1-11 <CHI>

A;Cross-references: UNIPROT:P04562  
C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting

C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyrog

P;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental

Query Match Score 21; DB 1; Length 11;  
Best Local Similarity 30.4%; Score 21; Pred. No. 1.3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PRPP 10  
DB 5 PSPP 9

## RESULT 9

B60274  
major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)

C;Species: Mycobacterium tuberculosis (fragment)  
C;Accession: B60274 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993

C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993

R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991  
A;Title: Isolation and partial characterization of major protein antigens in the culture

A;Reference number: A60274; MUID:91099989; PMID:1898899

A;Status: preliminary

A;Cross-references: UNIPROT:B60274

A;Molecule type: protein

A;Residues: 1-15 <NAG>

Query Match Score 20; DB 2; Length 5;  
Best Local Similarity 29.0%; Score 20; DB 2; Length 5;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPMP 8  
DB 4 DRAP 1

## RESULT 10

S10783  
enamelin f - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)  
C;Accession: S10783 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998

R;Strawich, E.; Glimcher, M.J.

Biochem. 191, 47-55, 1990  
A;Title: booch, enamelin' identified mainly as serum proteins. Major 'enamelin' is albu

A;Reference number: S10780; MUID:90336641; PMID:2379503

A;Cross-references: S10783

A;Molecule type: protein  
A;Residues: 1-8 <STR>

C;Keywords: enamel; phosphoprotein

Query Match Score 20; DB 2; Length 8;  
Best Local Similarity 25.0%; Score 20; DB 2; Length 8;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PRPP 9  
DB 5 PSPP 7

## RESULT 11

QY 6 PRPP 9  
DB 2 PLPP 5

Query Match Score 20; DB 1; Length 12;  
Best Local Similarity 29.0%; Score 20; DB 1; Length 12;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPMP 9  
DB 3 DBSAP 7

## RESULT 12

QY 6 PRPP 9  
DB 3 PVLP 6

Query Match Score 20; DB 2; Length 8;  
Best Local Similarity 29.0%; Score 20; DB 2; Length 8;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PRPP 9  
DB 3 PVLP 6

## RESULT 13

QY 6 PRPP 9  
DB 3 PVLP 6

Query Match Score 20; DB 1; Length 12;  
Best Local Similarity 29.0%; Score 20; DB 1; Length 12;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DPMP 9  
DB 3 DBSAP 7

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C;Accession: PN0663

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J.; Biochem, 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0663

A;Molecule type: protein

A;Residues: 1-12 &lt;YOS&gt;

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 29 0%; Score 20; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 1; Gaps 0;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TPPP 9  
Db 3 PLPP 6

## RESULT 14

B30572 T-cell receptor beta chain C region (CRRB29) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1989 #sequence\_revision 03-Apr-1989 #text\_change 30-May-1997

C;Accession: B30572

R;Williams, C.B.; Gutman, G.A.

J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utilization

A;Reference number: A30563; MUID:9110038; PMID:5563271

A;Accession: B30572

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-9 &lt;WIL&gt;

C;Keywords: T-cell receptor

Query Match 27.5%; Score 19; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TPP 9  
Db 7 TPP 9

## RESULT 15

A60108 exotoxin A - Streptococcus pyogenes (strain C203-S) (fragment)

N;Alternate name: blaserin A; scarlet fever toxin

C;Species: Streptococcus pyogenes

C;Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 09-Jul-2004

C;Accession: A60108

R;Schlievert, P.M.; Gray, E.D.

Infect. Immun. 57, 1865-1867, 1989

A;Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blast

A;Reference number: A60108; MUID:89254013; PMID:2498210

A;Accession: A60108

A;Molecule type: protein

A;Residues: 1-9 &lt;SCH&gt;

A;Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R311; UNIPROT:Q57453; UNIP

C;Keywords: exotoxin

Query Match 27.5%; Score 19; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTP 8  
Db 2 DDP 5Search completed: January 6, 2005, 11:27:11  
Job time : 39 secs

GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

## On protein - protein search, using SW model

Run on: January 6, 2005, 11:17:01 ; Search time 188 Seconds  
(without alignments)

36.726 Million cell updates/sec

Title: US-10-047-945-4  
Perfect score: 69  
Sequence: 1 LKAMDPTPPLWI 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched:

1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02;\*  
1: uniprot\_sprot;\*  
2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	27	39.1	7	1 TPFFY PACDA	P83455 pachymedusa
2	27	39.1	10	1 TMOF AEDAB	P19425 aedes aegypti
3	26.7	11	2 Q9UEI1	Q9UCL1 homo sapien	
4	25	36.2	12	2 Q6X7V1	Q6XV11 canis familiaris
5	25	36.2	12	2 Q8KZ86	Q8IZ86 acinetobacter
6	25	36.2	12	2 Q8KZ919	Q8P7919 canis familiaris
7	24	34.8	8	2 Q7MLV6	Q7MLV6 solanum tuberosum
8	23	33.3	10	2 Q76WKS	Q76WKS eurypharynx
9	23	33.3	10	2 Q8B7160	Bab87160 eurypharynx
10	23	33.3	11	2 Q8IVC8	Q8IVC8 homo sapien
11	23	33.3	11	2 Q8A33464	Caa33464 homo sapien
12	22	31.9	11	2 Q8M4Z1	Q8M4Z1 maripa paniculata
13	22	31.9	11	2 Q8WMA23	Q8WMA23 maripa repeana
14	22	31.9	11	2 Q8WM339	Q8WM339 wilsonia huachucae
15	22	31.9	11	2 Q8WMS58	Q8WMS58 seddera hirsutissima
16	22	31.9	11	2 Q8MB77	Q8MB77 odonellia hispida
17	22	31.9	11	2 Q8MB79	Q8MB79 aniseia argentea
18	22	31.9	11	2 Q8MB97	Q8MB97 maripa paniculata
19	22	31.9	11	2 Q8MBE1	Q8MBE1 ipomoea alba
20	21	30.4	6	1 E0101 LITRU	P83096 litoria rubra
21	21	30.4	9	2 Q9H326	Q9H326 homo sapien
22	21	30.4	9	2 Q6SP94	Q6SP94 chlamydomonas
23	21	30.4	9	2 Q99193	Q99193 pseudomonas
24	21	30.4	9	2 Q9PR4	Q9PR4 lepidostreus
25	21	30.4	9	2 AAR20844	Aar20844 chlamydomonas
26	21	30.4	10	1 BRK_ONCMY	Q9RZ11 oncorthynchus
27	21	30.4	10	1 URE3 MORMY	P17339 morganella morganii
28	21	30.4	10	2 P81859	P81898 prunus dulcis
29	21	30.4	11	1 BPP_AKGHP	P04562 agkistrodon
30	21	30.4	11	2 Q77956	Q77895 oreochromis
31	21	30.4	12	2 Q47251	Q47251 escherichia

## ALIGNMENTS

RESULT 1

ID	TPPF_PACDA	STANDARD;	PRT;	7 AA.
AC	P83455;			
DT	28-FEB-2003	(Rel. 41, Created)		
DT	05-JUL-2004	(Rel. 44, Last sequence update)		
OS	Tryptophyllin-1 (Pdt-1)			
OC	Eukaryota; Metacozia; Chordata; Craniata; Vertebrata; Butteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Phylomedusinae; Pachymedusa.			
RN	[1] NCBI_TaxID:75988;			
RP	SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF TISSUE-SKIN SECRETION;			
RC	Chen T.B., Orr D.F., Shaw C.,			
RT	"Pachymedusa dacnicolor tryptophyllin-1 (Pdt-1): structural characterization, pharmacological activity and cloning of precursor cDNA"; Submitted (SRB-2002) to Swiss-Prot.			
RL	-1- FUNCTION: Myoactive. Has Selective relaxing activity on vascular smooth muscle. SUBCELLULAR LOCATION: Secreted.			
CC	-1- SUBCELLULAR LOCATION: Skin. TISSUE_SPECIFICITY: Skin.			
CC	-1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.			
DR	GO; GO-0005576; C:extracellular; NAS; GO; GO-004586; R:negative regulation of smooth muscle contraction; R:Amidation; Amphibian defense peptide; Direct protein sequencing; KW:Hydroxylation.			
FT	FT MOD_RES 3 3 Hydroxyproline.			
FT	FT MOD_RES 7 7 Proline amide.			
SO	SEQUENCE 7 AA: 794 MW: 7772037D07776350 CIR64;			

RESULT 2

Qy	8 PPLWI 12	8 PPLWI 12	8 PPLWI 12
Oy	Db	Db	Db
	2 PPAWV 6	2 PPAWV 6	2 PPAWV 6

Query Match Best Local Similarity 60.0%; Pred. No. 1.8e+05; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
 OX NCBI\_TAXID=7159;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=eero beach; TISSUE=Ovary;  
 RX MEDLINE=930367888; PubMed=2393318;  
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
 RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like  
 enzyme biosynthesis in the midgut.";  
 RL FASEB J. 4:3015-3020(1990).  
 RN [2]  
 RP SEQUENCE.  
 RC STRAIN=vero beach; TISSUE=Ovary;  
 RX MEDLINE=83357794; PubMed=8355256;  
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
 RT "Mass spectrometry and characterization of Aedes aegypti t-tryptin  
 modulating oostatic factor (TMOF) and its analogs.;"  
 RL Insect Biochem. Mol. Biol. 23: 703-712(1993).  
 CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis  
 in the midgut which indirectly reduces the vitellogenin  
 concentration in the hemolymph resulting in inhibition of oocyte  
 development.  
 CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular  
 epithelium 18-24 hrs after a blood meal. Synthesis peaks at 36 hrs  
 CC and stops at 56 hrs.  
 DR PIR; A345454; A36454.  
 KW Direct protein sequencing; Hormone.  
 FT DOMAIN 3 10 YD -> DY IN TMFO(B).  
 FT VARIANT 1 2 POLY-Pro.  
 SQ SEQUENCE 10 AA; 1047 MW; 236D05777776DC7 CRC64;

Query Match 39.1%; Score 27; DB 1; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 1; ID 0;

OY 5 DPTPP 9  
 Db 2 DPAPP 6

RESULT 3

OYQRI PRELIMINARY; PRT; 11 AA.  
 ID QPCR1;  
 AC 01-MAY-2000 (TREMBUREL. 13, Created)  
 DT 01-MAY-2000 (TREMBUREL. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBUREL. 21, Last annotation update)  
 DB AUTOTAXIN (Fragment).  
 OS Homo sapiens (Human);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92129337; PubMed=1733949;  
 RA Stracke M.L., Krutschach H.C., Unsworth B.J., Arrestad A., Cioce V.,  
 RA Schiffmann B., Liotta L.A.;  
 RT "Identification, purification, and partial sequence analysis of  
 autotaxin, a novel motility-stimulating protein.";  
 RL J. Biol. Chem. 267:2524-2529(1992).  
 FT NON\_TER 1 11 1111 MW; 2723615AA043773 CRC64;  
 SQ SEQUENCE 11 AA; 1171 MW;

Query Match 37.7%; Score 26; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; ID 0;

OY 9 PLWI 12  
 Db 4 PLWI 7

RESULT 4

ID Q6X7V1 PRELIMINARY; PRT; 12 AA.  
 ID Q6X7V1 PRELIMINARY; PRT; 12 AA.  
 AC 06X7V1,  
 DT 05-JUL-2004 (TREMBUREL. 27, Created)  
 DT 05-JUL-2004 (TREMBUREL. 27, Last annotation update)  
 DE Insulin-like factor 3 (Fragment).  
 RT Name=INSI3;  
 OS Canis familiaris (Dog).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;  
 OC NCBI\_TAXID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22939740; PubMed=12890727;  
 RA Truong A., Bogatcheva N.V., Scheiling C., Dolf G., Agoulnik A.I.;  
 RT "Isolation and expression analysis of the canine insulin-like factor 3  
 gene," Reprod. 69:1658-1664(2003).  
 RL EMBL; AY251015; AAP79619; 1; -;  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1354 MW; 20ED91ADFA7DD737 CRC64;

Query Match 36.2%; Score 25; DB 2; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 2.6e+03; 0; Mismatches 4; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 MDPTPLW 11  
 Db 1 MSPRLAW 8

RESULT 5

ID Q8KZ66 PRELIMINARY; PRT; 12 AA.  
 ID Q8KZ66 PRELIMINARY; PRT; 12 AA.  
 AC 08KZ66;  
 DT 01-OCT-2002 (TREMBUREL. 22, Created)  
 DT 01-OCT-2002 (TREMBUREL. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBUREL. 22, Last annotation update)  
 DB Class I integron DNA integrase (Fragment).  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2220987; PubMed=12284388;  
 RA Gombac F., Riccio M.L., Rossolini G.M., Lagatolla C., Tonin E.,  
 RA Monti-Bragadin C., Lavenia A., Dolzani L.;  
 RT "Molecular characterization of integrons in epidemiologically  
 unrelated clinical isolates of *Acinetobacter baumannii* from Italian  
 hospitals reveals a limited diversity of gene cassette arrays.;"  
 RT RL Antimicrob. Agents Chemother. 46:3665-3668(2002).  
 DR EMBL; AUJ1334; CAC8591; 1; -;  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1295 MW; 90426B8FEE376DC1 CRC64;

Query Match 36.2%; Score 25; DB 2; Length 12;  
 Best Local Similarity 62.5%; Pred. No. 2.6e+03; 0; Mismatches 3; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 AMDPPEPL 10  
 Db 4 ATAPLEPPL 11

RESULT 6

ID AAP79619 PRELIMINARY; PRT; 12 AA.  
 ID AAP79619 PRELIMINARY; PRT; 12 AA.  
 AC AAP79619;  
 DT 02-MAR-2004 (TREMBUREL. 27, Created)

DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)

DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)

DE Insulin-like factor 3 (Fragment).

GN INSL3.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=12890727;

RT "Isolation and Expression Analysis of the Canine Insulin-Like Factor 3 Gene"; Biol. Reprod. 69:1658-1664(2003).

RL EMBL; AY251015; AAP79619.1; -.

DR NON\_TER 12 12

FT SEQUENCE 12 AA; 1354 MW; 20SD91ADFA7DD737 CRC64;

SQ Query Match 36.2%; Score 25; DB 2; Length 12; Best Local Similarity 50.0%; Pred. No. 2.6e+03; Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 MDPTPP 11

Db 1 MSRPLAW 8

RESULT 7

ID Q7M1V6 PRELIMINARY; PRT; 8 AA.

AC 07M1V6;

DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DB Lectin (Fragment).

OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Lamiales; Solanales; Solanaceae; Solanum.

NCBI\_TaxID=4113;

[1]

RP SEQUENCE.

RA Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R., Millar G.P.;

RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization, immunolocalization and effects of wounding.";

RL Blochim. J. 283:813-821(1992).

DR PIR; S21288; S21288.

FT NON\_TER 1 1

FT NON\_TER 8 8

SQ SEQUENCE 8 AA; 771 MW; C37775A771B5BDDA CRC64;

Query Match 34.8%; Score 24; DB 2; Length 8; Best Local Similarity 57.1%; Pred. No. 1.8e+06; Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AMDPTPP 9

Db 2 ASTFSPP 8

RESULT 8

ID Q76MK5 PRELIMINARY; PRT; 10 AA.

AC 076MK5;

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DB ATPase subunit 8 (Fragment).

GN Name=ATPase 8;

OS Eurypharynx pelecanoides (pelican eel).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Eurypterygidae; Eurypharynx.

OC NCBI\_TaxID=55117;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=22367687; PubMed=12949142;

RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR GO; GO:0005739; C:mitochondrion; IBA.

KW Mitochondrion.

FT NON\_TER 10 10

SQ SEQUENCE FROM N.A.

RT Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;

RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";

RL Mol. Biol. Evol. 20:1917-1924(2003).

RN [2]

RP SEQUENCE FROM N.A.

RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR GO; GO:0005739; C:mitochondrion; IBA.

KW Mitochondrion.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

RT Query Match 33.3%; Score 23; DB 2; Length 10; Best Local Similarity 60.0%; Pred. No. 4.5e+03; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPTP 8

Db 4 LDPSP 8

RESULT 9

ID BAB87160 PRELIMINARY; PRT; 10 AA.

AC BAB87160;

DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)

DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)

DB ATPase subunit 8 (Fragment).

GN ATPASE 8.

OS Eurypharynx pelecanoides (pelican eel).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Eurypterygidae; Eurypharynx.

OC NCBI\_TaxID=55117;

RN [1]

RP SEQUENCE FROM N.A.

RC Inoue J.G., Miya M., Tsukamoto K., Nishida M.;

RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels.";

RT Mol. Biol. Evol. 20:1917-1924(2003).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=D;

RT Inoue J.G., Miya M., Tsukamoto K., Nishida M.;

RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels.";

RT Mol. Biol. Evol. 20:1917-1924(2003).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=D;

RT Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;

RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB046487; BAB87160.1; -.

KW Mitochondrion.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1217 MW; D99C5E75A76AA736 CRC64;

Query Match 33.3%; Score 23; DB 2; Length 10; Best Local Similarity 60.0%; Pred. No. 4.5e+03; Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPTP 8

Db 4 LDPSP 8

RESULT 10

Q8IVG8

ID	Q8IVG8	PRELIMINARY;	PRT;	11 AA.	Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
AC	Q8IVG8;				Qy	7	TPPL	10						
DT	01-MAR-2003	(TREMBrel. 23; Created)			Db	3	TPPL	6						
DT	01-MAR-2003	(TREMBrel. 23; Last sequence update)												
DT	05-JUL-2004	(TREMBrel. 27; Last annotation update)												
DB	low density lipoprotein receptor related protein 1 (lipoprotein receptor-related protein) (Fragment).													
GN	Name=LRP;													
GN	Homo sapiens (Human);													
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;													
OC	Mammalia; Buteria; Primates; Catarrhini; Hominoidea; Homo.													
OX														
RN	NCBI_TaxID=9056;													
RP	[1] TISSUE=Blood;													
RC	TISSUE=Blood;													
RA	Glaeser C.;													
RL	Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.													
RN														
RP	SEQUENCE FROM N.A.													
RC	TISSUE=Leukoocyte;													
RX	Medline=9008395; PubMed=2597675;													
Kuett H.C., Herz J., Stanley K.K.;														
RT	*structure of the low-density lipoprotein receptor-related protein (LRP) Promoter.;													
RL	Biochim. Biophys. Acta 1009:229-236(1999).													
DR	EMLB: Y18524; CAD: 7169_1; -.													
DR	EMLB: X15424; CAA33464_1; -.													
DR	GO; GO:0004872; Fireceptor activity; IFA.													
KW	Lipoprotein; Receptor;													
FT	NON_TER 11 11 11 AA; 1221 MW; 373D041E27273777 CRC64;													
SQ														
Query Match 33.3%; Score 23; DB 2; Length 11; Best Local Similarity 100.0%; Pred. No. 5e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy	7	TPPL	10	Db	3	TPPL	6						
RESULT 11														
CA33464														
ID	CA33464	PRELIMINARY;	PRT;	11 AA.										
AC	Q8MAZ1													
DT	02-MAR-2004 (TREMBrel. 27; Created)													
DT	02-MAR-2004 (TREMBrel. 27; Last sequence update)													
DT	02-MAR-2004 (TREMBrel. 27; Last annotation update)													
DB	Lipoprotein receptor-related protein (Fragment).													
GN														
OS	Homo sapiens (Human);													
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;													
OC	Mammalia; Buteria; Primates; Catarrhini; Hominoidea; Homo.													
OX														
RN	NCBI_TaxID=9056;													
RP	SEQUENCE FROM N.A.													
RC	TISSUE=Leukoocyte;													
RA	Kuett H.C., Herz J., Stanley K.K.;													
RT	*structure of the low-density lipoprotein receptor-related protein (LRP) Promoter.;													
RT	Biochim. Biophys. Acta 1009:229-236(1999).													
RL														
DR	EMLB: X15424; CAA33464_1; -.													
DR	GO; GO:0009507; Chloroplast; IEA.													
KW	Chloroplast.													
FT	NON_TER 11 11 1260 MW; 9373D59440861B1 CRC64;													
SQ														
Query Match 31.9%; Score 22; DB 2; Length 11; Best Local Similarity 100.0%; Pred. No. 7.3e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy	7	TPPL	10	Db	3	TPPL	6						

QY	9	PLW	11
Db	9	PLW	11
QY	9	PLW	11
Db	9	PLW	11

Search completed: January 6, 2005, 11:26:28  
Job time : 191 SECs

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CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, CC Addison's disease or Hodgkin's disease) or depression. The efficacy of CC the protein may be monitored by assaying a human endogenous protein by CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva CC collection is relatively non-invasive when compared to blood collection CC for serum. Saliva can be centrifuged immediately, whereas blood requires CC clotting time before centrifugation to separate serum. Saliva proteins CC can be assayed by a simple ELISA test, whereas an assay of proteins from CC serum requires a more complicated sandwich type ELISA.

SQ Sequence 12 AA;

Query	Match	Score	DB	Length
Best	Local Similarity	100.0%	7	12
Matches	Conservative	100.0%	0	0
OY			0.00032	0
Db	1 LKAMDPTPPM 12			
	1 LKAMDPTPPM 12			

RESULT 2

ID ABB80226

ID ABB80226 standard; peptide; 11 AA.

AC XX

AC ABB80226;

DT 06-NOV-2003 (first entry)

XX DB

DB Synthetic LTNF, LT-11.

XX KW lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;

KW IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;

KW ADA; diabetes; autoimmune disease; Systemic lupus erythematosus;

KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;

KW Graves' disease; Addison's disease; Hodgkin's disease; depression;

KW saliva; ELISA.

XX OS Synthetic.

XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PF 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US-00047945.

XX PA (LIPP/ ) LIPPS B V.

XX PA (LIPP/ ) LIPPS F W.

XX PI Lipps BV, Lipps FW; (LIPP/ ) LIPPS F W.

XX DR WPI; 1998-271108/24.

PT As saying a human endogenous protein (e.g. IGF, nerve growth factor, PT insulin or adenosine deaminase or myoglobin), useful for diagnosing, e.g. PT asthma or diabetes, by employing an ELISA on a saliva sample from a patient.

XX PS Claim 7; Page 4; 24pp; English.

The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by

CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva CC sample using an anti-serum that is specific for the protein. Saliva CC collection is relatively non-invasive when compared to blood collection CC for serum. Saliva can be centrifuged immediately, whereas blood requires CC clotting time before centrifugation to separate serum. Saliva proteins CC can be assayed by a simple ELISA test, whereas an assay of proteins from CC serum requires a more complicated sandwich type ELISA.

SQ Sequence 11 AA;

Query	Match	Score	DB	Length
Best	Local Similarity	100.0%	7	11
Matches	Conservative	100.0%	0	0
OY			0.0013	0
Db	1 LKAMDPTPPW 11			
	1 LKAMDPTPPW 11			

RESULT 3

ID AAW53843

ID AAW53843 standard; peptide; 10 AA.

AC XX

AC AAW53843;

DT 08-JUL-1998 (first entry)

XX DE N-terminus of opossum LTNP.

XX KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;

KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;

KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;

XX OS Didelphis virginiana.

XX PN US5744443-A.

XX PD 28-APR-1998.

XX PR 03-JUN-1996; 96US-006557163.

XX PR 10-MAY-1993; 93US-00058387.

XX PR 22-SEP-1994; 94US-00310340.

XX PA (LIPP/ ) LIPPS B V.

XX PA (LIPP/ ) LIPPS F W.

XX PI Lipps FW, Lipps BV;

XX DR WPI; 1998-271108/24.

PT Lethal Toxin Neutralising Factor peptide from opossum - can neutralise PT venom(s) from all major families of poisonous snakes.

XX PS Claim 7; Col 11; 11pp; English.

XX CC This sequence represents the peptide of the invention. It is a Lethal CC Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic CC protein derived from an opossum. The peptide can be used in a method for CC treating a victim of envenomation from a poisonous snake, preferably a CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It CC is useful for the treatment of snake bites, sepsis, allergies caused by CC the environment and treatment of bee or scorpion stings or toxicities CC caused by plant or bacterial toxins. The peptide can also be used in CC histamine reaction treatment. The peptide can be used in envenomation CC treatment for a variety of snakes without prior identification of the CC snake. Being short it can be synthetically prepared rather than the CC current production in horses, where some people can show hypersensitivity CC to horse proteins

SQ Sequence 10 AA;





KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PI 10-APR-2002; 2002WO-US011654.  
 PR 25-APR-2001; 2001US-0283112P.  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 25-APR-2001; 2001US-0283112P.  
 PR 10-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSY INC.  
 XX  
 PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;  
 DR Morrison K, Morrison RK, Raitano AB;  
 XX  
 WPI; 2003-075555/07.

PT New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

PT New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

PS Claim 13, Page 232, 1021pp; English.

CC The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

SQ Sequence 9 AA;

Query Match	Score	DB	Length
Best Local Similarity	59.4%	6	9
Matches	6	Pred. No.	1.7e+06
		Mismatches	1
		Indels	0
		Gaps	0

QY 4 MDPPPLWI 12  
 DB 1 MDPSVPIWI 9

RESULT 9

ID ABR12854  
 AC ABR12854;  
 DT 19-MAY-2003 (first entry)  
 DB Human cancer-related protein 156P1D4 HLA peptide #978.  
 KW Human, cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 PR 10-APR-2002; 2002WO-US011654.  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSY INC.  
 XX  
 PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;  
 PR Morrison K, Morrison RK, Raitano AB;  
 XX  
 WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 PR 10-APR-2002; 2002WO-US011654.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSY INC.  
 XX  
 PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;  
 PR Morrison K, Morrison RK, Raitano AB;  
 XX  
 WPI; 2003-075555/07.

CC The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

SQ Sequence 9 AA;

Query Match	Score	DB	Length
Best Local Similarity	59.4%	6	9
Matches	6	Pred. No.	1.7e+06
		Mismatches	1
		Indels	0
		Gaps	0

QY 4 MDPPPLWI 12  
 DB 1 MDPSVPIWI 9

RESULT 10

ID ABR12743  
 AC ABR12743 standard; peptide; 10 AA.  
 XX  
 AC ABR12743;  
 XX  
 DT 19-MAY-2003 (first entry)  
 DB Human cancer-related protein 156P1D4 HLA peptide #978.  
 KW Human, cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 PR 10-APR-2002; 2002WO-US011654.  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 XX  
 PA (AGEN-) AGENSY INC.  
 XX  
 PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;  
 PR Morrison K, Morrison RK, Raitano AB;  
 XX  
 WO200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 PR 10-APR-2002; 2002WO-US011654.

DR WPI; 2003-075555/07.

XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX  
PS Claim 13, Page 239; 1021pp; English.

The present invention relates to novel human cancer-related genes and  
proteins (ABZ8120-ABZ78168 and ABR01789-ABR01861). The genes and  
proteins are useful for eliciting a humoral or cellular immune response.  
The genes are useful as probes and primers for the amplification and/or  
detection of genes, mRNAs or their fragments, as reagents for the  
diagnosis and/or prognosis of cancer, as coding sequences capable of  
directing the expression of the protein, as tools for modulating or  
inhibiting the expression of genes and/or translation of transcripts, and  
as therapeutic agents. The proteins and peptides are useful as  
therapeutic, prognostic and diagnostic reagents for cancer. The present  
sequence is a human leukocyte antigen (HLA) peptide, used in an example  
from the invention

SQ Sequence 10 AA;

Query	Match	Score	DB	Length
Best Local Matches	6; Conservative	41;	6;	10;
Matches	2;	Pred. No.	-7.5;	
Indels	1;	Mismatches		
Gaps	0;			

OY 1 4 MDPTPPLWI 12

Db 1 MDPSVPIWI 9

RESULT 11

ABR11875;  
ID ABR11875 standard; peptide; 10 AA.

AC ABR11875;

DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 156P1D4 HLA peptide #110.

KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

OS Homo sapiens.

XX WO200283921-A2.

XX PN

XX PD

24-OCT-2002.

XX PP 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSY INC.

XX PT Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;

PT Morrison K, Morrison RK, Raitano AB;

DR WPI; 2003-075555/07.

XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX  
PS Claim 13; Page 233; 1021pp; English.

CC proteins (ABZ8120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention

SQ Sequence 10 AA;

Query	Match	Score	DB	Length
Best Local Matches	6; Conservative	41;	6;	10;
Matches	2;	Pred. No.	7.5;	
Indels	1;	Mismatches		
Gaps	0;			

OY 4 MDPTPPLWI 12

Db 2 MDPSVPIWI 10

RESULT 12

ABR12121  
ID ABR12121 standard; peptide; 10 AA.  
XX AC ABR12121;  
XX DT 19-MAY-2003 (first entry)

XX DE Human cancer-related protein 156P1D4 HLA peptide #356.

XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283921-A2.

XX PD 24-OCT-2002.

XX PP 10-APR-2002; 2002WO-US011654.

XX PR 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX PA (AGEN-) AGENSY INC.

XX PT Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;

PT Morrison K, Morrison RK, Raitano AB;

DR WPI; 2003-075555/07.

XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.

XX  
PS Claim 13, Page 231; 1021pp; English.

XX  
The present invention relates to novel human cancer-related genes and

CC from the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 59.4%; Score 41; DB 6; Length 10;  
 Best Local Similarity 65.7%; Pred. No. 7.5;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 MDPTPPLWI 12  
 DB 1 1 MDPSVPIWI 9

RESULT 13  
 ABR12948  
 ID ABR12948 standard; peptide; 10 AA.  
 XX  
 AC ABR12948,  
 XX  
 DT 19-MAY-2003 (first entry)  
 DB Human cancer-related protein 156P1D4 HLA peptide #1183.  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 OS Homo sapiens.  
 XX  
 PN WO200283921-A2.  
 PD 24-OCT-2002.  
 PR 10-APR-2002; 2002WO-US011654.  
 PR 10-APR-2002; 2002WO-US011654.  
 PR 10-APR-2001; 2001US-0282739P.  
 PR 10-APR-2001; 2001US-0283112P.  
 PR 25-APR-2001; 2001US-0286630P.  
 PA (AGEN-) AGENSY INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Farris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.

XX  
 PT New composition comprising a substance that modulates the structure of proteins and polynucleotides useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

XX  
 PT New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients.

XX  
 PS Claim 13; Page 233; 1021PP; English.

XX  
 CC The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The protein and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

XX  
 SQ Sequence 10 AA;

Query Match 59.4%; Score 41; DB 6; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 7.5;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 MDPTPPLWI 12  
 DB 2 MDPSVPIWI 10

RESULT 15  
 ABR12294  
 ID ABR12294 standard; peptide; 10 AA.  
 XX  
 AC ABR12294;  
 XX  
 DT 19-MAY-2003 (first entry)

QY 4 MDPTPPLWI 12  
 DB 1 MDPSVPIWI 9

XX  
DE Human cancer-related protein 156P1D4 HLA peptide #529.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002; 2002WO-US011654.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
PR 10-APR-2001; 2001US-0283112P.  
PR 25-APR-2001; 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYN INC.  
XX  
PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI; 2003-075555/07.  
XX  
PS Claim 13, Page 235, 1021pp; English.  
XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
RS  
The present invention relates to novel human cancer-related genes and  
CC proteins (AB278120-AB278168 and AB01783-AB01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
Sequence 10 AA:

Query Match 59.4%; Score 41; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 7.5;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	4	MDPTPPLWI	12
DB	2	MDPSVPIWI	10

Search completed: January 6, 2005, 11:23:12  
Job time : 154 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 6, 2005, 11:26:37 ; Search time 140 Seconds

30.906 Million cell updates/sec

Title: US-10-047-945-4  
Perfect score: 69  
Sequence: 1 LKAMDPTPPLWI 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 210148

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
\*

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2: /cgmn_6/ptodata/1/pubpa/PCT_NEW_PUB.pep:*
3: /cgmn_6/ptodata/1/pubpa/US06_PUBCOMB.pep:*
4: /cgmn_6/ptodata/1/pubpa/US06_PUBCOMB.pep:*
5: /cgmn_6/ptodata/1/pubpa/US07_NEW_PUB.pep:*
6: /cgmn_6/ptodata/1/pubpa/RECUTS_PUBCOMB.pep:*
7: /cgmn_6/ptodata/1/pubpa/US08_NEW_PUB.pep:*
8: /cgmn_6/ptodata/1/pubpa/US08_PUBCOMB.pep:*
9: /cgmn_6/ptodata/1/pubpa/US09A_PUBCOMB.pep:*
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17: /cgmn_6/ptodata/1/pubpa/US10_EU_PUB.pep:*
18: /cgmn_6/ptodata/1/pubpa/US11_NEW_PUB.pep:*
19: /cgmn_6/ptodata/1/pubpa/US60_NEW_PUB.pep:*
20: /cgmn_6/ptodata/1/pubpa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	69	100.0	12	14	US-10-047-945-4
2	65	94.2	11	14	US-10-047-945-5
3	54	78.3	10	14	US-10-047-945-1
4	50	72.5	9	14	US-10-047-945-6
5	43	62.3	8	14	US-10-047-945-7
6	34	49.3	12	16	US-10-327-735
7	32	46.4	12	14	US-10-186-815-6
8	32	46.4	12	14	US-10-161-791-252
9	32	46.4	12	14	US-10-116-275-52
10	31	44.9	9	17	US-10-611-440-188
11	30	43.5	8	15	US-10-437-708-168
12	30	43.5	8	17	US-10-257-199-168
13	30	43.5	10	14	US-10-190-082-480

Sequence 480, App

RESULT 1  
US-10-047-945-4  
; Sequence 4, Application US/10047945  
; Publication No. US20030157552A1  
; GENERAL INFORMATION  
; APPLICANT: LIPPS, FREDERICK W.  
; APPLICANT: LIPPS, BINIE V.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (19E) IMPLICATED DISORDERS  
; FILE REFERENCE: F1MPAT015US  
; CURRENT APPLICATION NUMBER: US/10/047-945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR FILING NUMBER:  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.  
US-10-047-945-4  
Query Match 100.0%; Score 69; DB 14; length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0011; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;  
Qy 1 LKAMDPTPPLWI 12  
Db 1 LKAMDPTPPLWI 12

RESULT 2

US-10-047-945-5  
; Sequence 5, Application US/10047945  
; Publication No. US20030157555AI  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (19B) IMPLICATED DISORDERS  
; FILE REFERENCE: FWPAT0105US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; PRIORITY CLAIM:  
; PRIORITY FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.

US-10-047-945-5  
Query Match 94.2%; Score 65; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0041; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 1 LKAMDPTPPW 11  
Db 1 LKAMDPTPPW 11

RESULT 3  
US-10-047-945-1  
; Sequence 1, Application US/10047945  
; Publication No. US20030157555AI  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (19B) IMPLICATED DISORDERS  
; FILE REFERENCE: FWPAT0105US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.

US-10-047-945-1  
Query Match 94.2%; Score 65; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0041; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 1 LKAMDPTPPW 11  
Db 1 LKAMDPTPPW 11

RESULT 5  
US-10-047-945-7  
; Sequence 7, Application US/10047945  
; Publication No. US20030157555AI  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (19B) IMPLICATED DISORDERS  
; FILE REFERENCE: FWPAT0105US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
; SEQ ID NO 7  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.

US-10-047-945-7  
Query Match 72.5%; Score 50; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 1 LKAMDPTPP 9  
Db 1 LKAMDPTPP 9

RESULT 6  
US-10-327-598-735  
; Sequence 735, Application US/10327598  
; Publication No. US20040181039AI  
; GENERAL INFORMATION:  
; APPLICANT: Krah, Eugene

RESULT 4  
US-10-047-945-6  
; Sequence 6, Application US/10047945

RESULT 5  
US-10-047-945-5  
; Sequence 5, Application US/10047945

RESULT 6  
US-10-327-598-735  
; Sequence 735, Application US/10327598  
; Publication No. US20040181039AI  
; GENERAL INFORMATION:  
; APPLICANT: Krah, Eugene



Query Match 46.4%; Score 32; DB 14; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DPTPP 9  
 Db 5 DPTPP 9

RESULT 10  
 US-10-611-440-188  
 ; Sequence 188, Application US/10/11440  
 ; Publication No. US20040197912A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Berinstein, Neil  
 ; APPLICANT: Gallichan, Scott  
 ; APPLICANT: Lovitt, Corey  
 ; APPLICANT: Parrington, Mark  
 ; APPLICANT: Pedyczak, Artur  
 ; APPLICANT: Radvanyi, Laszlo  
 ; APPLICANT: Singh-Sandhu, Devender  
 ; APPLICANT: Oomen, Raymond P  
 ; APPLICANT: Cao, Shi-Xian  
 ; TITLE OF INVENTION: Tumor Antigens BRA4 and BCY1 for Prevention and/or Treatment of  
 ; TITLE OF INVENTION: Cancer  
 ; FILE REFERENCE: API-2-11-US  
 ; CURRENT APPLICATION NUMBER: US/10/611,440  
 ; CURRENT FILING DATE: 2003-07-01  
 ; PRIOR APPLICATION NUMBER: US 60/394,346  
 ; PRIOR FILING DATE: 2002-07-03  
 ; PRIOR APPLICATION NUMBER: US 60/394,503  
 ; PRIOR FILING DATE: 2002-07-09  
 ; PRIOR APPLICATION NUMBER: US 60/411,833  
 ; PRIOR FILING DATE: 2002-09-18  
 ; PRIOR APPLICATION NUMBER: US 60/445,342  
 ; PRIOR FILING DATE: 2003-02-06  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 188  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: CLP-2825  
 ; US-10-611-440-188

Query Match 44.9%; Score 31; DB 17; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+06; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPPLW 11.  
 Db 2 ETSPLWLW 8

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RESULT 11  
 US-10-437-708-168  
 ; Sequence 168, Application US/10/37708  
 ; Publication No. US2004000555A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kieliszewski, Marcia  
 ; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
 ; TITER OF INVENTION: Glycoproteins  
 ; PUBLISHER: OHU-04089  
 ; CURRENT APPLICATION NUMBER: US/10/437,708  
 ; CURRENT FILING DATE: 2003-05-14  
 ; PRIOR APPLICATION NUMBER: US/09/547,693  
 ; PRIOR FILING DATE: 2000-04-12  
 ; NUMBER OF SEQ ID NOS: 236  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 168  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 ; FEATURE:  
 ; LOCATION: (1)..(1)  
 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (3)..(4)  
 ; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

US-10-257-199-168  
 ; Sequence 168, Application US/10/257199  
 ; Publication No. US20040230032A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kieliszewski, Marcia  
 ; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
 ; TITLE OF INVENTION: Glycoproteins  
 ; FILE REFERENCE: OHU-06319  
 ; CURRENT APPLICATION NUMBER: US/10/257,199  
 ; CURRENT FILING DATE: 2003-05-09  
 ; PRIOR APPLICATION NUMBER: 09/547,693  
 ; PRIOR FILING DATE: 2000-04-12  
 ; NUMBER OF SEQ ID NOS: 244  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 168  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 ; FEATURE:  
 ; LOCATION: (1)..(1)  
 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (3)..(4)  
 ; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

RESULT 13  
 US-10-190-082-480  
 ; Sequence 480, Application US/10/190082  
 ; Publication No. US20030148264A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lasky, Lawrence A.  
 ; APPLICANT: Sridhar, Sachdev S.  
 ; APPLICANT: Heid, Heike A.  
 ; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS

```

FILE REFERENCE: P1905RL ; APPLICANT: Kieliszewski, Marcia
; CURRENT APPLICATION NUMBER: US/10/190,082 ; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
; CURRENT FILING DATE: 2002-07-03 ; TITER OF INVENTION: Glycoproteins
; PRIOR APPLICATION NUMBER: US 60/303,634 ; FILE REFERENCE: OHO-06319
; CURRENT FILING DATE: 2001-07-06 ; CURRENT APPLICATION NUMBER: US/10/257,199
; NUMBER OF SEQ ID NOS: 683 ; CURRENT FILING DATE: 2003-05-09
; SEQ ID NO 480 ; PRIOR APPLICATION NUMBER: 09/547,693
; LENGTH: 10 ; NUMBER OF SEQ ID NOS: 244
; TYPE: PRT ; SOFTWARE: Patent version 3.0
; ORGANISM: Artificial sequence ; SEQ ID NO 165
; FEATURE: ; LENGTH: 10
; OTHER INFORMATION: Synthetic ; TYPE: PRT
; US-10-190-082-480 ; ORGANISM: Artificial Sequence
; Sequence 15, Application US/10437708 ; FEATURE:
; Publication No. US2004000555A1 ; OTHER INFORMATION: Synthetic
; GENERAL INFORMATION: ; FEATURE:
; APPLICANT: Kieliszewski, Marcia ; NAME/KEY: SITE
; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich ; LOCATION: (1)..(1)
; FILE REFERENCE: OHO-04089 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; CURRENT APPLICATION NUMBER: US/10/437,708 ; NAME/KEY: SITE
; CURRENT FILING DATE: 2003-05-14 ; LOCATION: (3)..(3)
; PRIOR APPLICATION NUMBER: US/09/547,693 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; PRIOR FILING DATE: 2000-04-12 ; FEATURE:
; NUMBER OF SEQ ID NOS: 236 ; NAME/KEY: SITE
; SOFTWARE: PatentIn version 3.0 ; LOCATION: (5)..(6)
; SEQ ID NO 165 ; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
; LENGTH: 10 ; QUERY MATCH
; TYPE: PRT ; Best Local Similarity 43.5%; Score 30; DB 14; Length 10;
; ORGANISM: Artificial/Unknown ; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; FEATURE: ; NAME/KEY: misc_feature
; NAME/KEY: misc_feature ; OTHER INFORMATION: Synthetic
; FEATURE: ; FEATURE:
; NAME/KEY: SITE ; LOCATION: (1)..(1)
; LOCATION: (1)..(1) ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE: ; NAME/KEY: SITE
; NAME/KEY: SITE ; LOCATION: (3)..(3)
; LOCATION: (3)..(3) ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; OTHER INFORMATION: The Proline at this position is a hydroxyproline.
; FEATURE: ; NAME/KEY: SITE
; NAME/KEY: SITE ; LOCATION: (5)..(6)
; LOCATION: (5)..(6) ; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.
; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.

RESULT 14
Query Match 43.5%; Score 30; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.5e+02; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
NAME/KEY: SITE
; OTHER INFORMATION: Synthetic
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-437-708-165

RESULT 14
Query Match 43.5%; Score 30; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.5e+02; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
NAME/KEY: SITE
; OTHER INFORMATION: Synthetic
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-437-708-165

RESULT 15
Query Match 43.5%; Score 30; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NAME/KEY: SITE
; OTHER INFORMATION: Synthetic
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-437-708-165

Query Match 43.5%; Score 30; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
NAME/KEY: SITE
; OTHER INFORMATION: Synthetic
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-437-708-165

RESULT 15
US-10-257-199-165
; Sequence 15, Application US/10257199
; Publication No. US20040230032A1
; GENERAL INFORMATION:

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Gencore version 5.1.6

OM protein - protein search, using SW model

Run on: January 6, 2005, 11:18:11 ; Search time 38 Seconds  
                   ( without alignments )  
                   20.943 Million cell updates/sec

Title: US-10-047-945-4  
       Perfect score: 69  
       Sequence: 1 LKAMDPFPPLWI 12

Scoring table: BLOSUM62  
       Gapop 10.0 , Gapext: 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0  
       Maximum DB seq length: 12

Post-processing: Minimum Match 10%  
       Maximum Match 100%  
       Listing first 45 summaries

Database : Issued\_Patents\_AH:\*\*

- 1: /cgn12\_6/ptodata/1/iaa/5A\_COMB.pep:\*\*
- 2: /cgn12\_6/ptodata/1/iaa/5B\_COMB.pep:\*\*
- 3: /cgn12\_6/ptodata/1/iaa/6A\_COMB.pep:\*\*
- 4: /cgn12\_6/ptodata/1/iaa/6B\_COMB.pep:\*\*
- 5: /cgn12\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*\*
- 6: /cgn12\_6/ptodata/1/iaa/backfile1.pep:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	54	78.3	10	1 US-08-657-163A-2
2	32	46.4	11	US-08-657-163A-2
3	32	46.4	11	US-08-657-877-31
4	32	46.4	11	US-08-476-515A-31
5	32	46.4	12	US-08-603-252
6	32	46.4	12	US-08-500-124-252
7	30	43.5	6	US-08-232-446B-24
8	30	43.5	8	US-09-547-693-168
9	30	43.5	10	US-09-547-693-165
10	29	42.0	12	US-09-311-926A-18
11	28	40.6	10	US-09-131-341-7
12	28	40.6	10	US-09-739-852-7
13	27	39.1	6	US-08-989-290-2
14	27	39.1	6	US-07-698-2
15	27	39.1	6	US-08-468-596-2
16	27	39.1	6	US-03-298-996B-12
17	27	39.1	6	US-03-291-846B-15
18	27	39.1	6	US-09-551-737C-15
19	27	39.1	6	US-03-291-924B-2
20	27	39.1	6	US-03-551-738B-12
21	27	39.1	7	US-07-99-290-3
22	27	39.1	7	US-08-271-698-3
23	27	39.1	7	US-03-291-846B-13
24	27	39.1	7	US-09-455-996B-13
25	27	39.1	7	US-03-295-846B-16
26	27	39.1	7	US-03-551-737C-16
27	39.1	7	4	US-09-295-924B-3

**ALIGNMENTS**

RESULT 1  
       US-08-657-163A-2

```

; Sequence 2, Application US/08657163A
; Patent No. 574449
; GENERAL INFORMATION:
; APPLICANT: BINIR V. LIPPS AND FREDERICK W. LIPPS
; TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND
; TITLE OF INVENTION: SYNTHETIC LTNFS AND THEIR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BINIR V. LIPPS
; STREET: 4505 MIMOSA DR.
; CITY: BELLAIRE
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1
; SOFTWARE: MS WORD 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,163A
; FILING DATE:
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/310,340
; FILING DATE: 22 SEPTEMBER 1994
; CLASSIFICATION: 514
; APPLICATION NUMBER: 08/058,387
; FILING DATE: 10 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN R. CASPERSON
; REGISTRATION NUMBER: 28,198
; REFERENCE/DOCKET NUMBER: FWL-PAT-US-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-482-2961
; TELEFAX: 713-663-7290
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: AMINO ACID
; STRANDBNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N
;
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; ORIGINAL SOURCE: SYNTHETIC  
US-08-657-163A-2

APPLICANT: Hjalm, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

Query Match 78.3%; score 54; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy	Dy
1	1
LKAMDPPTPL	LKAMDPPTPL
10	10

NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd., 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:  
MEDIMM NUMBER: 51000000000000000000

US-08-336-343A-31  
Sequence 31, Application US/08336343A  
Patent No. 567714  
GENERAL INFORMATION:  
APPLICANT: Ulrich, Axel  
TITLE OF INVENTION: CCT-2, A NO. 567714el Receptor Tyrosine Kinase  
NUMBER OF SENTENCES: 41

**CORRESPONDENCE ADDRESSES:**  
**ADDRESSEE:** Pennie & Edmonds  
**STREET:** 1155 Avenue of the Americas  
**CITY:** New York  
**STATE:** New York  
**Country:** U.S.A.  
**ZIP:** 10036-2711

**COMPUTER READABLE FORM:**  
MEDIUM: TYPE: P10000 A1000

PRIOR APPLICATION NUMBER: F51US95/15200  
PRIOR APPLICATION DATE: 22-NOV-1995  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,314  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
SANTO, G. -

CONFIDENTIALITY: None  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/336,343A

NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355B-U  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808

**CLASSIFICATION:** 435  
**ATTORNEY/AGENT INFORMATION:**  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 6783-065-  
**TELECOMMUNICATION INFORMATION:**  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO:  
 SEQUENCE CHARACTERISTICS  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 PROHIBITED MOTIFS: internal

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPIC: unknown

FRAGMENTS: LITERATE  
9-652-877-31

MOLECULAR TYPE: peptide  
B-336-343A-31

2 KAMDPTPPL 10

```

      Every Match       Score 32; DB 1; Length 11;
      Local Similarity 66.4%; Pred. No. 40;
      Matches 6; Conservative 0; Mismatches 3; Indels 0; Caps 0

```

3 KMPRPL 11

2	KAMDPTPP <sub>L</sub>	10
1		
3	KMPPPRPP <sub>L</sub>	11

4  
3-476-515A-31  
Sequence 31, Application US/08476515A  
tent No. 6239270  
**GENERAL INFORMATION:**

LT 3  
8-6503-977-21

GENERAL INFORMATION:  
APPLICANT: Åkerblom, Goran  
APPLICANT: Jublin, Claes  
APPLICANT: Rask, Lars

STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;  
 STREET: 3C43;  
 CITY: Collegeville  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19426-0107  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Compaq PC  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: Word 7.0 (Patentin)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/476,515A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/344,836  
 FILING DATE: 23-NOV-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/SE94/00483  
 FILING DATE: 24-MAY-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: SB 9301764-8  
 FILING DATE: 24-MAY-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Savitzky, Martin  
 REGISTRATION NUMBER: 29,699  
 REFERENCE/DOCKET NUMBER: A1355D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-454-3808  
 TELEFAX: 610-454-3816  
 INFORMATION FOR SEQ ID NO: 31:  
 INFORMATION FOR SEQ ID NO: 252:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 FRAGMENT TYPE: internal  
 US-08-476-515A-31

Query Match 46.4%; Score 32; DB 3; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 40;  
 Matches 6; Conservative 0; Mismatches 3;  
 Qy 2 KAMDPPTPL 10  
 Db 3 KPMPPRPL 11

RESULT 5  
 US-08-602-999A-252  
 ; Sequence 252, Application US/09500124  
 ; Patent No. 6433920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DBR, Channing J.  
 ; APPLICANT: FOWLER, Dana M.  
 ; APPLICANT: RIDER, James E.  
 TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 NUMBER OF SEQUENCES: 467  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/500,124  
 FILING DATE:  
 CLASSIFICATION:  
 APPLICATION NUMBER: 09/602,999  
 FILING DATE: 16-FEB-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Misrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 1101-202  
 TELECOMMUNICATION INFORMATION:

Query Match 46.4%; Score 32; DB 3; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 44;  
 Matches 6; Conservative 0; Mismatches 3;  
 Qy 2 KAMDPPTPL 10  
 Db 3 KPMPPRPL 11

RESULT 6  
 US-09-500-124-252  
 ; Sequence 252, Application US/09500124  
 ; Patent No. 6433920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DBR, Channing J.  
 ; APPLICANT: FOWLER, Dana M.  
 ; APPLICANT: RIDER, James E.  
 TITLE OF INVENTION: ISOLATING AND USING SAME  
 NUMBER OF SEQUENCES: 467  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/500,124  
 FILING DATE:  
 CLASSIFICATION:  
 APPLICATION NUMBER: 09/602,999  
 FILING DATE: 16-FEB-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Misrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 1101-202  
 TELECOMMUNICATION INFORMATION:

Query Match 46.4%; Score 32; DB 3; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 40;  
 Matches 6; Conservative 0; Mismatches 3;  
 Qy 2 KAMDPPTPL 10  
 Db 3 KPMPPRPL 11

RESULT 5  
 US-08-602-999A-252  
 ; Sequence 252, Application US/09500124  
 ; Patent No. 6433920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DBR, Channing J.  
 ; APPLICANT: FOWLER, Dana M.  
 ; APPLICANT: RIDER, James E.  
 TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 NUMBER OF SEQUENCES: 467  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/500,124  
 FILING DATE:  
 CLASSIFICATION:  
 APPLICATION NUMBER: 09/602,999  
 FILING DATE: 16-FEB-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Misrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 1101-202  
 TELECOMMUNICATION INFORMATION:

Query Match 46.4%; Score 32; DB 3; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 40;  
 Matches 6; Conservative 0; Mismatches 3;  
 Qy 2 KAMDPPTPL 10  
 Db 3 KPMPPRPL 11

TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 INFORMATION FOR SEQ ID NO: 252:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 TOPOGY: unknown  
 MOLECULE TYPE: peptide  
 US-09-500-124-252

Query Match		Score 32; DB 4; Length 12;	
Best Local Similarity 66.7%; Pred. No. 44;		Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Qy	2 KAMDPPTPPL 10	Db	4 KENPPRPL 12

RESULT 7  
 US-09-232-446B-24  
 Sequence 24, Application US/09232446B  
 ; Patent No. 6228647  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gai, Xiaowu  
 ; TITLE OF INVENTION: Transposable Element Protein that Directs DNA  
 ; TITLE OF INVENTION: Integration to Specific Chromosomal Sites  
 ; FILE REFERENCE: 2-98  
 ; CURRENT APPLICATION NUMBER: US/09/232,446B  
 ; CURRENT FILING DATE: 1999-01-15  
 ; PRIOR APPLICATION NUMBER: US 60/071,383  
 ; PRIOR FILING DATE: 1998-01-15  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 24  
 ; LENGTH: 6  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: mutant peptide  
 ; OTHER INFORMATION: Sequence  
 US-09-232-446B-24

Query Match		Score 30; DB 3; Length 6;	
Best Local Similarity 66.7%; Pred. No. 3.8e+05;		Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
Qy	4 MDPTPP 9	Db	1 LDPSPP 6

RESULT 8  
 US-09-547-693-168  
 Sequence 168, Application US/09547693  
 ; Patent No. 6639050  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kieliszewski, Marcia  
 ; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
 ; FILE REFERENCE: OHU-04089  
 ; CURRENT APPLICATION NUMBER: US/09/547,693  
 ; CURRENT FILING DATE: 2000-04-12  
 ; NUMBER OF SEQ ID NOS: 236  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 168  
 ; LENGTH: 6

Query Match		Score 30; DB 3; Length 6;	
Best Local Similarity 66.7%; Pred. No. 3.8e+05;		Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
Qy	4 MDPTPP 9	Db	1 LDPSPP 6

RESULT 9  
 US-09-547-693-165  
 Sequence 165, Application US/09547693  
 ; Patent No. 6639050  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kieliszewski, Marcia  
 ; TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich  
 ; FILE REFERENCE: OHU-04089  
 ; CURRENT APPLICATION NUMBER: US/09/547,693  
 ; CURRENT FILING DATE: 2000-04-12  
 ; NUMBER OF SEQ ID NOS: 236  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 165  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial/Unknown  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: SYNTHETIC  
 ; NAME/KEY: SITE  
 ; LOCATION: (1)..(1)  
 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
 ; NAME/KEY: SITE  
 ; LOCATION: (3)..(3)  
 ; OTHER INFORMATION: The Proline at this position is a hydroxyproline.  
 ; LOCATION: (5)..(6)  
 ; OTHER INFORMATION: The Proline at these positions is a hydroxyproline.  
 US-09-547-693-165

Query Match		Score 30; DB 4; Length 10;	
Best Local Similarity 100.0%; Pred. No. 76;		Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	6 PTTPPL 10	Db	3 PTTPPL 7

RESULT 10  
 US-09-315-926A-18  
 Sequence 18, Application US/0931526A  
 ; Patent No. 6498027  
 ; GENERAL INFORMATION:  
 ; APPLICANT: B's van, Helmut  
 ; APPLICANT: Havenga, Menzo  
 ; APPLICANT: Verlinden, Stefan  
 ; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER  
 ; FILE REFERENCE: 2193-40500US  
 ; CURRENT APPLICATION NUMBER: US/09/315,926A  
 ; CURRENT FILING DATE: 1999-05-20  
 ; PRIOR APPLICATION NUMBER: EP 99201593.3  
 ; PRIOR FILING DATE: 1999-05-20  
 ; PRIOR APPLICATION NUMBER: EP 98201693.3  
 ; NAME/KEY: misc\_feature

PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 18  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: misc feature  
; OTHER INFORMATION: Description of Artificial Sequence: phage display peptide

US-09-315-926A-18

Query Match 42.0%; Score 29; DB 4; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02; 1; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 1; Db 0; Qy 0;

Qy 7 TPPPLW 11  
Db 7 TPPAW 11

RESULT 11

US-09-133-341-7 Application US/09133341A  
Patient No. 616240  
GENERAL INFORMATION:  
APPLICANT: Hayward, Diane S.  
APPLICANT: Ling, Paul D.  
TITLE OF INVENTION: BNA2 PEPTIDES AND METHODS OF USING SAME  
FILE REFERENCE: 87512  
CURRENT APPLICATION NUMBER: US/09/133,341A  
CURRENT FILING DATE: 1998-08-13  
EARLIER APPLICATION NUMBER: WO 97052243  
EARLIER FILING DATE: 1997-02-12  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 7  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE: .  
OTHER INFORMATION: Description of Unknown Virus Organism: Artificial

US-09-133-341-7

Query Match 40.6%; Score 28; DB 3; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02; 1; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 2; Db 0; Qy 0;

Qy 6 PTTPPLW 11  
Db 2 PGPPWW 7

RESULT 12

US-09-739-852-7 Application US/09739852  
Sequence 7, Application US/09739852  
Patient No. 6495144  
GENERAL INFORMATION:  
APPLICANT: Hayward, Diane S.  
APPLICANT: Ling, Paul D.  
TITLE OF INVENTION: BNA2 PEPTIDES AND METHODS OF USING SAME  
FILE REFERENCE: 87512  
CURRENT APPLICATION NUMBER: US/09/739,852  
CURRENT FILING DATE: 2000-12-18  
PRIORITY APPLICATION NUMBER: 09/133,341  
PRIOR FILING DATE: 2000-12-18  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 7  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE: .

RESULT 13

US-07-989-290-2 Application US/07989290  
Sequence 2, Application US/07989290  
Patient No. 5358934  
GENERAL INFORMATION:  
APPLICANT: Borovsky, Dov  
APPLICANT: Carlson, David A.  
TITLE OF INVENTION: Materials and Methods for Control  
TITLE OF INVENTION: Materials and Methods for Control  
TITLE OF INVENTION: Materials and Methods for Control  
NUMBER OF SEQ ID NOS: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Salivanchik  
STREET: 2421 NW. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/989,290  
FILING DATE: 19921211  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Salivanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: UP/SAS-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5600  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: AMINO ACID  
STRANDBEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-989-290-2

RESULT 14

US-08-271-698-2 Application US/08271698  
Sequence 2, Application US/08271698  
Patient No. 549821  
GENERAL INFORMATION:  
APPLICANT: Borovsky, Dov  
APPLICANT: Carlson, David A.  
TITLE OF INVENTION: Materials and Methods for Control

TITLE OF INVENTION: of Pests  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 STATE: FL USA  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/271,698  
 FILING DATE: 07-JUL-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/989,290  
 FILING DATE: 11-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: UP/S&S-127  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 2:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 STRANDEDNESS: single  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYDROPHOBICITY: HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-271-698-2

RESULT 15  
 US-08-468-596-2  
 Sequence 2, Application US/08468596  
 Patent No. 5629196  
 GENERAL INFORMATION:  
 APPLICANT: Borovsky, Dov  
 APPLICANT: Carlson, David A.  
 TITLE OF INVENTION: Materials and Methods for Control  
 TITLE OF INVENTION: of Pests  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 STATE: FL USA  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/468,596  
 FILING DATE: 06-JUN-1995

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/271,698  
 FILING DATE: 07-JUL-1994  
 APPLICATION NUMBER: US/07/989,290  
 FILING DATE: 11-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: UP/S&S-127  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 STRANDEDNESS: single  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYDROPHOBICITY: HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-468-596-2

Query Match 39.1%; Score 27; DB 1; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 3.8e+05; Mismatches 1; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; MisMatch 1; Indel 0; Gap 0;

Qy	5 DPTPP 9	Db	2 DPAPP 6

Search completed: January 6, 2005, 11:27:54  
 Job time : 38 SECs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 6, 2005, 10:09:21 ; Search time 15.6757 Seconds  
 (without alignments)  
 61.380 Million cell updates/sec

Title: US-10-047-945-1  
 Perfect score: 54  
 Sequence: 1 LKAMDPPTPPL 10

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79,\*  
 1: pir1,\*  
 2: pir2,\*  
 3: pir3,\*  
 4: pir4,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	77.8	398	2	A81717	conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain Nigg)
2	38	70.4	792	2	T29187	probable nucleoporin
3	38	70.4	1325	2	S62497	similar to transcrip-
4	37	68.5	142	2	A8181	hypothetical prote-
5	37	68.5	212	2	C87585	alpha-1-B-glycopro-
6	37	68.5	237	2	A42013	hypothetical prote-
7	37	68.5	286	2	S7384	tailless (tl1) pro-
8	37	68.5	429	2	S09852	hypothetical prote-
9	37	68.5	450	2	B47765	tailless (tl1) pro-
10	37	68.5	452	2	A3502	hypothetical prote-
11	37	68.5	1819	2	T32008	hypothetical protein C55C3.3 - Caenorhabditis elegans
12	36	66.7	117	2	AF3119	CIDate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
13	36	66.7	222	2	T71955	CAccession: T29187
14	36	66.7	365	2	F87552	R.Woessner, J.; Stellies, L.
15	36	66.7	392	2	T29119	submitted to the EMBL Data Library, April 1996
16	36	66.7	431	2	T29716	A.Description: The sequence of C. elegans cosmid C55C3.
17	36	66.7	460	2	H70986	A.Reference number: Z220585
18	36	66.7	490	2	T49096	A.Accession: T29187
19	36	66.7	898	2	T21179	A.Status: preliminary; translated from GB/EMBL/DDJB
20	36	66.7	944	2	A89524	A.Molecule type: DNA
21	36	66.7	968	2	T46568	A.Residues: 1-792 <WOR>
22	36	66.7	2717	2	A3203	A.Cross-references: EMBL:U53335; PTID:AAA96170.1; GSPDB:GN00022; CESP:C55C3.3
23	35	64.8	159	2	S61040	A.Experimental source: strain Bristol N2; clone C55C3
24	35	64.8	206	2	S50913	C.Species:
25	35	64.8	262	2	E6479	A.Gene: CESP:C55C3.3
26	35	64.8	291	2	AH2017	A.Map Position: 4
27	35	64.8	313	2	A19559	A.Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 4
28	35	64.8	323	1	TWVTF	probable membrane protein kinase - Ye
29	35	64.8	380	1	TVFVFM	tryptophan synthase
						lipoic acid synthase
						conserved hypothetical protein kinase
						protein kinase (EC
						protein kinase (EC
						probable protein k
						cytochrome P450-BF
						succinate dehydro-
						protein kinase (EC
						hypothetical prote-
						protein kinase raf
						protein kinase raf
						beta-glucuronidase
						protein P84 - huma
						probable vacuolar
						chitinase - Strept
						immediate-early pr
						hypothetical prote-

## ALIGNMENTS

RESULT 1  
 A81717  
 conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain Nigg)  
 C.Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
 C.Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 CAccession: A81717  
 R.Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg Nucleic Acids Res, 28, 1397-1405, 2000  
 A.Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
 A.Reference: A81500; MUID:20150255; PMID:10684935  
 A.Accession: A81717  
 A.Status: preliminary  
 A.Molecule type: DNA  
 A.Residues: 1-398 <TEN>  
 A.Cross-references: UNIPROT:Q93L02; GB:AB002298; GB:AE002160; NID:9719343; PIDN:AAF391.  
 A.Experimental source: strain Nigg (Mopn)  
 C.Genetics:  
 C.Gene: TCI306  
 C/Superfamily: Chlamydia trachomatis hypothetical protein CR036

RESULT 2  
 Query Match 77.8%; Score 42; DB 2; Length 398;  
 Best Local Similarity 77.8%; Pred. No. 8.4; Mismatches 1; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Pairs 0;  
 Qy 2 KAMDPPTPPL 10  
 Db 309 KELDPTPPL 317

Query Match 77.8%; Score 42; DB 2; Length 398;  
 Best Local Similarity 77.8%; Pred. No. 8.4; Mismatches 1; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Pairs 0;  
 Qy 2 KAMDPPTPPL 10  
 Db 309 KELDPTPPL 317

hypothetical protein C55C3.3 - Caenorhabditis elegans  
 C.Species: Caenorhabditis elegans  
 C.Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 CAccession: T29187  
 R.Woessner, J.; Stellies, L.

submitted to the EMBL Data Library, April 1996

A.Description: The sequence of C. elegans cosmid C55C3.

A.Reference number: Z220585

A.Accession: T29187

A.Status: preliminary; translated from GB/EMBL/DDJB

A.Molecule type: DNA

A.Residues: 1-792 <WOR>

A.Cross-references: EMBL:U53335; PTID:AAA96170.1; GSPDB:GN00022; CESP:C55C3.3

A.Experimental source: strain Bristol N2; clone C55C3

C.Species:

A.Gene: CESP:C55C3.3

A.Map Position: 4

A.Introns: 17/1; 46/3; 139/2; 173/1; 204/3; 250/3; 266/3; 286/2; 327/1; 362/3; 393/3; 4

probable membrane protein kinase - Ye

tryptophan synthase

lipoic acid synthase

conserved hypothetical protein kinase

protein kinase (EC

		Best Local Similarity 87.5%; Pred. No. 93; Matches 7; Conservative 0; Mismatches 1; Db 133	Qy 1 LKAMDPPTP 8	Qy 1 LKAMDPPTP 9
Qy	1	LKAMDPPTP 8		
Db	133	LKAMDPPTP 140	130	LKAMDPPTP 138
				RESULT 5
		S62497		C87585
		probable nucleoporin - fission yeast (Schizosaccharomyces pombe)		hypothetical protein CC2714 [imported] - Caulobacter crescentus
		C;Species: Schizosaccharomyces pombe		C;Species: Caulobacter crescentus
		C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004		C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
		C;Accession: S62497; T38281		C;Accession: C87585
		R;Niblett, D.; Harris, D.; Barrell, B.G.; Rejandream, M.A.; Walsh, S.V.		R;Nierman, W.C.; Raldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, n., J.; Embleva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
		submitted to the EMBL Data Library, October 1995		A;Title: Complete Genome Sequence of Caulobacter crescentus.
		A;Reference number: S62492		A;Reference number: A87249; MUID:21173698; PMID:11259647
		A;Accession: S62497		A;Accession: C87585
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: DNA		A;Molecule type: DNA
		A;Residues: 1-1325 <NTB>		A;Residues: 1-212 <STO>
		A;Cross-references: UNIPROT:Q09847; EMBL:Z64354; NID:91039338; PIDN:CAA91241.1; PID:9103		A;Cross-references: UNIPROT:Q9AWI; GB:AE005673; NID:913424303; PIDN:AAK24679.1; GSPDB:G-C;Genetic:
		R;Niblett, D.; Harris, D.; Barrell, B.G.; Rejandream, M.A.; Walsh, S.V.		A;Gene: CCA2714
		submitted to the EMBL Data Library, October 1995		A;Gene: CCA2714
		A;Reference number: Z21783		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Accession: T38281		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Status: preliminary; translated from GB/EMBL/DDJB		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Molecule type: DNA		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Residues: 1-1325 <NTB>		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Cross-references: EMBL:Z64354; PIDN:CAA91241.1; GSPDB:GN00066; SPDB:SPAC23D3.06C		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Experimental source: strain 972h-; cosmid c23D3		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		C;Genetics:		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Gene: SPAC23D3.06C		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Map position: 1R		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Introns: 33/3		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		RESULT 4		RESULT 6
		Query Match Similarity 70.4%; Score 38; DB 2; Length 1325; Best Local Similarity 87.5%; Pred. No. 1.7e+02; Mismatches 7; Conservative 0; Indels 0; Gaps 0; Db 299 KADPTPP 306		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		Similar o transcription regulators lin1991 [imported] - Listeria innocua (strain Clip112		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		C;Species: Listeria innocua		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		C;Accession: AE1681		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		Science 294, 849-852, 2001		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Mauko, C.; Schlueter, T.; Simoes, N.; Terrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.;Title: Comparative Genomics of Listeria species.		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Reference number: AB1077; MUID:21537279; PMID:11679669		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Accession: AE1681		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Stccus: preliminary		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Molecule type: DNA		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Residues: 1-142 <GLA>		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Cross-references: UNIPROT:Q92AD1; GB:AL592022; PIDN:CAC97221.1; PID:gi16414492; GSPDB:G-C;Experimental source: strain Clip11262		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		C;Genetics:		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		A;Gene: lin1991		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		C;Superfamily: conserved hypothetical protein MJ0568		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59
		Query Match Similarity 68.5%; Score 37; DB 2; Length 142; Best Local Similarity 77.8%; Pred. No. 20; Mismatches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Db 52 RSLDPTPP 59		Query Match Similarity 60.5%; Score 37; DB 2; Length 212; Best Local Similarity 62.5%; Pred. No. 32; Mismatches 5; Conservative 3; Indels 0; Gaps 0; Db 52 RSLDPTPP 59

RESULT 7

S72384 hypothetical protein 8 precursor - Enterococcus faecalis plasmid pAD1

C;Species: Enterococcus faecalis

C;Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004

C;Accession: S72384

R;Hart, H.; Wirth, R.; Muscholl, A.

A;Title: Comparative analysis of 18 sex pheromone plasmids from Enterococcus faecalis: d

A;Reference number: S72375; MUID:97074879; PMID:8917306

A;Accession: S72384

A;Molecule type: DNA

A;Residues: 1-286 <HIR>  
A;Cross-references: UNIPROT:Q4791; EMBL:X96977; NID:91279406; PIDN:CAA6567.1; PID:9127  
A;Experimental source: strain Ogix  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
C;Genetics:  
A;Genome: plasmid pADL  
C;Superfamily: probable pheromone-responsive protein  
P;1-265/Domain: signal sequence #status predicted <SIG>  
P;27-286/Product: hypothetical protein 8 #status predicted <MAT>  
Query Match      Best Local Similarity      Score 68.5%; Score 37; DB 2; Length 286;  
Matches      6; Conservative      1; Mismatches      2; Indels      0; Gaps      0;  
Qy      2 KAMDPPTPL 10  
Db      50 KRPDPTPPI 58

RESULT 8  
S09852 hypothetical protein U188 - human cytomegalovirus (strain AD169)  
C;Species: human cytomegalovirus, human herpesvirus 5  
A;Note: host Homo sapiens (man)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;  
M.; Barrell, B.G.  
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990  
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus  
A;Reference number: S09749; MUID:90269039; PMID:2161319  
A;Accession: S09852  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Residues: 1-429 <CHB>  
A;Cross-references: UNIPROT:PI6731; EMBL:X17403; NID:959591; PIDN:CAA35362.1; PID:917808  
A;Note: this sequence was submitted to the EMBL Data Library, December 1989

Query Match      Best Local Similarity      68.5%; Score 37; DB 2; Length 429;  
Matches      6; Conservative      2; Mismatches      1; Indels      0; Gaps      0;  
Qy      1 LIKAMDPPTPP 9  
Db      348 LRAALDPPP 356

RESULT 9  
B47265 tailless (tl) protein - fruit fly (*Drosophila virilis*)  
C;Species: *Drosophila virilis*  
C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-2004  
C;Accession: B47265  
R;Liu, G.J.; Steingrimsson, E.; Pignoni, F.; Courrey, A.J.; Lengyel, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 858-863, 1993  
A;Title: Characterization of downstream elements in a Raf-1 pathway.  
A;Reference number: A47265; MUID:93157371; PMID:8430097  
A;Accession: A47265  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-452 <LIA>  
A;Cross-references: UNIPROT:PI8102; GB:X52147  
R;Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courrey, A.J.; Lengyel, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 858-863, 1993  
A;Title: Characterization of downstream elements in a Raf-1 pathway.  
A;Reference number: A47265; MUID:93157371; PMID:8430097  
A;Accession: A47265  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-452 <LIA>  
A;Cross-references: UNIPROT:PI8102; GB:X52147  
R;Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courrey, A.J.; Lengyel, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 858-863, 1993  
A;Title: Characterization of downstream elements in a Raf-1 pathway.  
A;Reference number: A47265; MUID:93157371; PMID:8430097  
A;Accession: A47265  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-452 <LIA>  
A;Cross-references: UNIPROT:PI8102; GB:X52147  
R;Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courrey, A.J.; Lengyel, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 858-863, 1993  
A;Title: Characterization of downstream elements in a Raf-1 pathway.  
A;Reference number: A47265; MUID:93157371; PMID:8430097  
A;Accession: A47265  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-450 <LLM>  
A;Cross-references: GB:L04955  
C;Genetics:  
A;Gene: FLBase:Dvir-tll  
A;Cross-references: FLBase:FBgn0013145  
A;Superfamily: erba transforming protein homology  
C;Keywords: zinc finger transforming protein homology  
P;32-339/Domain: erba transforming protein homology <ERBA>

Query Match      Best Local Similarity      68.5%; Score 37; DB 2; Length 450;  
Matches      6; Conservative      2; Mismatches      1; Indels      0; Gaps      0;

RESULT 10  
A35602 tailless (tl) protein - fruit fly (*Drosophila melanogaster*)  
N;Alternative name: steroid hormone receptor homolog tl; transcription factor tl  
C;Species: *Drosophila melanogaster*  
C;Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: A35602; A47265  
R;Pignoni, F.; Baldarelli, R.M.; Steingrimsson, E.; Diaz, R.J.; Patapoutian, A.; Merriam, C.;Cell 62, 151-163, 1990  
A;Title: The *Drosophila* gene tailless is expressed at the embryonic termini and is a me...  
A;Reference number: A35602; MUID:90304905; PMID:2364433  
A;Accession: A35602  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-452 <PGG>  
A;Cross-references: UNIPROT:PI8102; GB:X52147  
R;Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courrey, A.J.; Lengyel, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 858-863, 1993  
A;Title: Characterization of downstream elements in a Raf-1 pathway.  
A;Reference number: A47265; MUID:93157371; PMID:8430097  
A;Accession: A47265  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-452 <LIA>  
A;Cross-references: UNIPROT:PI8102; GB:X52147  
R;Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courrey, A.J.; Lengyel, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 858-863, 1993  
A;Title: Characterization of downstream elements in a Raf-1 pathway.  
A;Reference number: A47265; MUID:93157371; PMID:8430097  
A;Accession: A47265  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-452 <LIA>  
A;Cross-references: UNIPROT:PI8102; GB:X52147  
R;Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courrey, A.J.; Lengyel, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 858-863, 1993  
A;Title: Characterization of downstream elements in a Raf-1 pathway.  
A;Reference number: A47265; MUID:93157371; PMID:8430097  
A;Accession: A47265  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-452 <LIA>  
A;Cross-references: UNIPROT:PI8102; GB:X52147  
R;Liaw, G.J.; Steingrimsson, E.; Pignoni, F.; Courrey, A.J.; Lengyel, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 858-863, 1993  
A;Title: Characterization of downstream elements in a Raf-1 pathway.  
A;Reference number: A47265; MUID:93157371; PMID:8430097  
A;Accession: A47265  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1819 <SRV>  
A;Cross-references: UNIPROT:O16625; EMBL:AF016669; PIDN:AAB66098.1; GSDB:GN00020; CBSP  
A;Experimental source: strain Bristol N2; clone K10G6  
C;Genetics:  
A;Gene: CBSP:K10G6.3  
A;Map Position: 2  
A;Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3  
Query Match      Best Local Similarity      68.5%; Score 37; DB 2; Length 1819;  
Matches      6; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

QY 1 LKAMDPTPP 9  
Db :||| 500 LMUDDPTPP 508

**RESULT 12**

AF3319 hypothetical protein BMRI0540 [imported] - *Brucella melitensis* (strain 16M)  
C;Species: *Brucella melitensis*  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C;Accession: AF3319  
R;DeiVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Lob, T.; Ivancova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzaz, P.H.; Magius, S.; O'Callaghan, D.; Letessier; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*  
A;Reference number: AD3252; PMID:11756688  
A;Accession: AF3319  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-117 <KUR>  
A;Cross-references: UNIPROT:Q8YIAs; GB:AE008917; PIDN:AAL51721.1; PID:gi17882457; GSPDB:G  
A;Experimental source: strain 16M  
C;Genetics:  
A;Gene: BMEI0540  
A;Map position: 1

Query Match 66.7%; Score 36; DB 2; Length 117;  
Best Local Similarity 66.7%; Pred. No. 24; Indels 2; Gaps 0;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPP 10  
Db :||| 83 KACDPLPPM 91

**RESULT 13**

C71955 hypothetical protein jhp0241 - *Helicobacter pylori* (strain J99)  
C;Species: *Helicobacter pylori*  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: C71955  
R;Alm, R.A.; Ling, L.S.H.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Voris, G.P.; Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MJD:99120557; PMID:9923602  
A;Accession: C71955  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-222 <ARN>  
A;Cross-references: UNIPROT:Q9ZMH9; GB:AE001462; GB:AB001439; NID:94154760; PIDN:AAD0583  
A;Experimental source: strain J99  
C;Genetics:  
A;Gene: jhp0241

Query Match 66.7%; Score 36; DB 2; Length 222;  
Best Local Similarity 75.0%; Pred. No. 50; Indels 2; Gaps 0;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPTPP 9  
Db :||| 193 KTIDDPTPP 200

**RESULT 14**

R87552 dprA protein [imported] - *Caulobacter crescentus*  
C;Species: *Caulobacter crescentus*  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C;Accession: R87552  
R;Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolod

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4116-4117, 2001  
A;Title: Complete Genome Sequence of *Caulobacter crescentus*.  
A;Reference number: A87249; MJD:21173698; PMID:11259647  
A;Accession: R87552  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-365 <STO>  
A;Cross-references: UNIPROT:Q9ASKO; GB:AE005673; NID:gi13423992; PIDN:AAK24418.1; GSPDB:G  
A;Gene: CC2447  
A;Map position: 1

Query Match 65.7%; Score 36; DB 2; Length 35;  
Best Local Similarity 60.0%; Pred. No. 88; Indels 2; Gaps 0;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LKAMDPTPP 10  
Db :||| 92 LAALDPPPV 101

**RESULT 15**

T29519 hypothetical protein T25F10.4 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T29519  
R;Pauley, A.; Gatting, S.; Submitted to the EMBL Data Library, July 1996  
A;Description: The sequence of *C. elegans* cosmid T25F10.  
A;Reference number: Z20634  
A;Accession: T29519  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-392 <PAU>  
A;Cross-references: UNIPROT:Q23048; EMBL:U64856; PIDN:AAB04987.1; GSPDB:GN00023; CESP:T2  
A;Experimental source: strain Bristol N2; clone T25F10  
C;Genetics:  
A;Gene: CESP:T25F10.4  
A;Map position: 5  
A;Introns: 38/3; 84/2; 156/3; 182/3; 228/3; 256/1; 312/2; 337/3; 361/2  
Query Match 66.7%; Score 36; DB 2; Length 392;  
Best Local Similarity 100.0%; Pred. No. 95; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DPTPP 10  
Db :||| 291 DPTPP 296

Search completed: January 6, 2005, 10:23:46  
Job time : 17.6757 secs

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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:00:35 ; Search time 85.6757 Seconds  
 (without alignments)  
 67.157 Million cell update/sec

<b>Title:</b>	US-10-047-945-1
<b>Sequence:</b>	1 LKAMDPTPPL 10
<b>Scoring table:</b>	BLOSUM62
<b>Searched:</b>	1825181 seqs, 575374646 residues
<b>Total number of hits satisfying chosen parameters:</b>	1825181
<b>Minimum DB seq length:</b>	0
<b>Maximum DB seq length:</b>	200000000
<b>Post-processing:</b>	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

Database : UniProt 02::\*

1: uniprot\_sprot;\*

2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	54	100.0	17	2	Q9TR78	Q9TR78 didelphis m
2	54	100.0	291	1	DM43 DIDMR	Q82957 didelphis m
3	45	83.3	140	2	Q8HZ75	Q8HZ75 didelphis m
4	45	83.3	291	2	Q8HZ74	Q8HZ74 didelphis m
5	42	77.8	398	1	Y306 CHLMU	Q9pl02 chlamydia m
6	41	99	99	2	Q6CS47	Q6CS47 kluyveromyces
7	41	75.9	165	2	Q9W3H5	Q9W3H5 drosophila
8	39	72.2	98	2	Q853J7	Q853J7 mycobacteri
9	39	72.2	156	2	Q8MLX6	Q8MLX6 echinococci
10	39	72.2	227	2	Q73ZB2	Q73ZB2 mycobacteri
11	39	72.2	227	2	AAS04008	AAS04008 mycobacte
12	39	72.2	243	2	Q961D3	Q961D3 homo sapien
13	39	72.2	268	2	Q6GIP6	Q6GIP6 bartonella
14	39	72.2	320	2	Q8V3M1	Q8V3M1 swinepox vi
15	39	72.2	693	2	Q9K437	Q9K437 streptomyce
16	39	72.2	754	1	KB15_HUMAN	Q9upn7 homo sapien
17	39	72.2	829	2	AAB02799	AAB02799 homo sapien
18	39	72.2	849	2	Q6NVJ7	Q6NVJ6 homo sapien
19	39	72.2	849	2	AAB68014	AAB68014 homo sapien
20	38	70.4	86	2	Q6FV03	Q6Fv03 candida gla
21	38	70.4	274	2	Q95Q06	Q95Q06 caenorhabdi
22	38	70.4	302	2	Q8CB43	Q8CB43 mus musculu
23	38	70.4	369	2	Q42606	Q42606 arabidopsis
24	38	70.4	563	2	Q95332	Q95332 arabidopsis
25	38	70.4	560	2	Q6CD9	Q6CD9 yarrowia li
26	38	70.4	881	2	Q9NE42	Q9NE42 leishmania
27	38	70.4	1326	2	Q9R642	Q9R642 schizosacch
28	38	70.4	1345	2	Q8CIP5	Q8CIP5 mus musculu
29	37	68.5	70	2	Q7PK7	Q7PK7 anopheles g
30	37	68.5	107	2	Q36604	Q36604 hepatitis e
31	37	68.5	142	1	MNTR_LISIN	MNTR_LISIN

RESULT 1

Query	Match	Length	DB	ID	Description
Q9TR78	100.0%	17	AA	RP	SEQUENCE.
Q9TR78	100.0%	17	AA	RP	MEDLINE-95149299; PubMed=7846694;
Q9TR78	100.0%	17	AA	RA	Perales J., Moussette H., Marrangoni S., Oliveira B., Domont G.B.;
Q9TR78	100.0%	17	AA	RT	"Isolation and partial characterization of an anti-bothropic complex from the serum of South American Didelphidae.";
Q9TR78	100.0%	17	AA	RT	Toxicon 32:1237-1249 (1994).
Q9TR78	100.0%	17	AA	RL	[1]
Q9TR78	100.0%	17	AA	RP	SEQUENCE.
Q9TR78	100.0%	17	AA	RP	MEDLINE-95149299; PubMed=7846694;
Q9TR78	100.0%	17	AA	RA	Perales J., Moussette H., Marrangoni S., Oliveira B., Domont G.B.;
Q9TR78	100.0%	17	AA	RT	"Isolation and partial characterization of an anti-bothropic complex from the serum of South American Didelphidae.";
Q9TR78	100.0%	17	AA	RT	Toxicon 32:1237-1249 (1994).
Q9TR78	100.0%	17	AA	RL	[1]
Q9TR78	100.0%	17	AA	RP	SEQUENCE.
Q9TR78	100.0%	17	AA	RP	MEDLINE-95149299; PubMed=7846694;
Q9TR78	100.0%	17	AA	RA	Perales J., Moussette H., Marrangoni S., Oliveira B., Domont G.B.;
Q9TR78	100.0%	17	AA	RT	"Isolation and partial characterization of an anti-bothropic complex from the serum of South American Didelphidae.";
Q9TR78	100.0%	17	AA	RT	Toxicon 32:1237-1249 (1994).
Q9TR78	100.0%	17	AA	RL	[1]
Q9TR78	100.0%	17	AA	RP	SEQUENCE, AND MASS SPECTROMETRY.
Q9TR78	100.0%	17	AA	RC	TISSUE=serum;
Q9TR78	100.0%	17	AA	RX	MEDLINE-2193368; PubMed=11815628; DOI=10.1074/jbc.M200589200;
Q9TR78	100.0%	17	AA	RA	Neves-Pereira A.G.C., Perales J., Fox J.W., Shannon J.D., Makino D.I., Garrett R.C., Domont G.B.,
Q9TR78	100.0%	17	AA	RA	"Structural and functional analyses of DM43, a snake venom metalloproteinase inhibitor from Didelphis marsupialis serum.;"
Q9TR78	100.0%	17	AA	RT	metalloproteinases inhibitor from Didelphis marsupialis serum.;"
Q9TR78	100.0%	17	AA	RL	J. Biol. Chem. 277:13128-13137 (2002).
Q9TR78	100.0%	17	AA	CC	-!- FUNCTION: Metalloproteinase inhibitor.
Q9TR78	100.0%	17	AA	CC	-!- SUBUNIT: Homodimer.
Q9TR78	100.0%	17	AA	CC	-!- TISSUE SPECIFICITY: Blood and milk.

ALIGNMENTS

CC -!- PTM: N-glycosylated.  
 CC -!- MASS SPECTROMETRY: MW=42691; METHOD=MALDI; RANGE=1-291;  
 CC NOTE=Ref.1.  
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like V-type domains.  
 DR InterPro; IPR07110; Ig-like.  
 DR InterPro; IPR011015; LEM-like.  
 DR PF00047; Ig; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 KW direct protein sequencing; Glycoprotein; Immunoglobulin domain;  
 Metalloprotease inhibitor; Repeat.  
 FT DOMAIN 114 171  
 DOMAIN 191 288  
 DOMAIN 28 74  
 FT CARBOHYD 213 265  
 FT CARBOHYD 23 23  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 175 175  
 SQ 291 AA; 32390 MW; 17A496227E69A65B CRC64;

Query Match 100.0%; Score 54; DB 1; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 47; 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LKAMDPPTPP 10  
 Db 1 LKAMDPPTPPL 10

RESULT 3  
 ID O8HZ75 PRELIMINARY; PRT; 140 AA.  
 AC O8HZ75; 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Alpha 1B glycoprotein DV0PS1-D (Fragment).  
 OC Didelphis marsupialis virginiana (North American opossum).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Didelphidae; Didelphimorphia; Didelphidae; Didelphis.  
 OX NCBI\_TAXID=9267;  
 [1] SEQUENCE FROM N.A.  
 DR Martinez M.B., Pierce J.R.; Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR InterPro; IPR011015; LEM\_like.  
 FT NON\_TER 1 1  
 FT SEQQUENCE 140 AA; 15297 MW; E19D071A76A5A7F CRC64;

Query Match 83.3%; Score 45; DB 2; Length 140;  
 Best Local Similarity 90.0%; Pred. No. 7.3%; 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LKAMDPPTPP 10  
 Db 42 LKAMDPPTPPL 51

RESULT 4  
 ID O8HZ74 PRELIMINARY; PRT; 291 AA.  
 AC O8HZ74; 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 26, Last annotation update)  
 DE Alpha 1B glycoprotein DV0P14 (Fragment).  
 OC Didelphis marsupialis virginiana (North American opossum).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Didelphidae; Didelphimorphia; Didelphidae; Didelphis.

OX NCBI\_TaxID=9267;  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Martinez M.E./ Pierce J.R./ Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AXJ31001; AN06912.1; -. DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR011015; LEM-like.  
 DR PFam; PF00047; Ig; 1.  
 DR PROSITE; PS50835; Ig\_LIKE; 1.  
 FT NON\_TER 1 1  
 FT SEQQUENCE 291 AA; 32509 MW; BBC282838A1C0BF4 CRC64;

Query Match 83.3%; Score 45; DB 2; Length 291;  
 Best Local Similarity 90.0%; Pred. No. 16; 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LKAMDPPTPPL 10  
 Db 1 LKAMDPPTPPL 10

RESULT 5  
 ID Y306\_CHLMU STANDARD; PRT; 398 AA.  
 AC O9P102; 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DR Hypothetical protein TC0306.  
 GN OrderredLocusNames=TC0306;  
 OS Chlamydia muridarum.  
 RC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TAXID=83560;  
 RP SEQUENCE FROM N.A.  
 RN [1]  
 RC STRAIN=MOPN / Nigg; MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Barry K.J.,  
 RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Cravent B.,  
 RA Dodson R.J., Gwynn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,  
 RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.,  
 RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
 pneumoniae AR39."; RT Nucleic Acids Res. 28:1397-1406(2000).  
 RA -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- SIMILARITY: Belongs to the chlamydial CPn0129/cp0367c0306 family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; AE002299; AMR39171.1; -. DR PIR; A81717; A81717.  
 DR TIGR; TC0306; -. DR Complete Proteome; Hypothetical protein; Transmembrane.  
 FT TRANSMEM 56 76  
 FT TRANSMEM 31 51 Potential.  
 FT SEQUENCE 398 AA; 44639 MW; 8CD8E541C5C92AB8 CRC64;

Query Match 77.8%; Score 42; DB 1; Length 398;  
 Best Local Similarity 77.8%; Pred. No. 76; 1; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY	2	KAMDPPTPPL	10	RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Db	309	KENDPTPPL	317	RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
DT	01-OCT-2004	(TREMBLREL_28, Created)		RA	Sutton G.G., Woottman J.R., Yandell M.D., Zhang Q., Chen L.X.,
DT	01-OCT-2004	(TREMBLREL_28, Last sequence update)		RA	Brandon R.C., Rogers B.H., Blazej R.G., Champé M., Pfeiffer B.D.,
DT	01-OCT-2004	(TREMBLREL_28, Last annotation update)		RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
DB	Similar to sgd S0007245	Saccharomyces cerevisiae YIL018ca COX19.		RA	Abrial J.F., Aghayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
GN	ORFNames=KLU00D039719;			RA	Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
OS	Kluyveromyces lactis (Yeast).			RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			RA	Borková D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
OK	Saccharomycetales; Saccharomycaceae; Kluyveromyces.			RA	Burtis K.C., Bumam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RN	[1] NEBI_TAXID=28985;			RA	Cherry J.M., Cauley S., Dahlke C., Davenport L.B., Davies P.,
RP	SEQUENCER FROM N.A.			RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RC	STRAIN=NRRL Y-1140;			RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RG	GENOMEVERS,			RA	Durbin R.K., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,
RA	Iafontaine L., de Montigny J., Marcq C., Neuville C., Tala B., V.,			RA	Foster C., Gabrielian A.B., Garg N.S., Galbart W.M., Glasser K.,
RA	Goffard N., Franclé L., Aigle M., Anthouard V., Barbe V.,			RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Barnay S., Blanchin S., Beckerich J.M., Beyne S., Bleijenberg C.,			RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Boisrame A., Boyer J., Cattolico L., Conflancieri F., de Daruvar A.,			RA	Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA	Bespans L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,			RA	Jalali M., Kalush F.A., Karpen G.H., Ke Z., Kemmink J.A., Kelchum K.A.,
RA	Hamravre P., Hennequin C., Janaiaux N., Joyet P., Kachouri R.,			RA	Kimmel B.R., Koikira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Kerrest A., Koszul R., Lemire M., Leut J., Ma L., Müller H.,			RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Nicauda J.M., Nikolski M., Ottas S., Ozier-Kalogeropoulos O.,			RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Pallenz S., Potier S., Richard G.F., Straub M.L., Suleau C.,			RA	Merkulov G., Mishina N.V., Molarry C., Morris J., Morris J., Mohrbacher A.,
RA	Swemere D., Tekija P., Wesołowski-Loulou M., Westhof S., Wirth B.,			RA	Mount S.M., Moy M., Murphy B., Murphy L., Muniz D.M., Nelson D.L.,
RA	Zenilou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,			RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA	Bouchier C., Caudron B., Scarpeilli C., Gaillardin C., Weissenbach J.,			RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G.,
RA	Wincker P., Souillet J.L., "Genome evolution in yeasts.",			RA	Reinert K., Remington K., Saunders R.D., Schneier P., Shen H.,
RT	Nature 430:35-44(2004).			RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RN	[2]			RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RP	SEQUENCE FROM N.A.			RA	Sirikas R., Tector C., Turner R., Venter C., Venter B., Wang A.H., Wang Y.,
RC	STRAIN=NRRL Y-1140;			RA	Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA	Genoscope;			RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.			RA	Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhou X., Smith H.O.,
DR	EML; CR382124; CRH00338.1; - .			RA	Zheng X.H., Zhong F.N., Zuong W., Zhou X., Zhu X., Smith H.O.,
SO	SEQUENCE 99 AA; 11050 MW; 032BA5DD3C50CAC2 CRC64;			RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Query	Query Match Similarity 75.9%; Score 41; DB 2; Length 99; Best Local Similarity 77.8%; Pid: No. 24; 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			RT	"The genome sequence of <i>Drosophila melanogaster</i> ,"
Qy	1 LKAMDPPTP	9		RT	Science 287:2185-2195(2000).
Db	9 LKALSPPTP 17			RN	[2]
RESULT 7				RP	SEQUENCE FROM N.A.
QW3H5	PRELIMINARY;	PRT;	165 AA.	RX	Medline=22426065; PubMed=12537568;
ID	QW3HS			RA	Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
AC	QW3HS_;			RA	Patel S., Adam M., Champe M., Dugan S.P., Frise E., Hodgson A.,
DT	01-MAY-2000	(TREMBLREL_13, Created)		RA	George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
DT	01-MAY-2000	(TREMBLREL_13, Last sequence update)		RA	Pacleb J.M., Park S., Pfefffer B.D., Richards S., Sodergren E.J.,
DT	01-JUL-2004	(TREMBLREL_27, Last annotation update)		RA	Svirskas R., Taiber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
DB	CG2147-PA (UP00728p).			RA	Weinstock G., Scherer S.E., Myers E.W., Gibbes R.A., Rubin G.M.,
GN	ORFNames=CG2147;			RT	"finishing a whole-genome shotgun: release 3 of the <i>Drosophila melanogaster</i> euchromatic genome sequence,"
OS	Drosophila melanogaster (Fruit fly).			RT	Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
OC	Drosophila; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Notoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Spidozoidea; Drosophilidae; Drosophila.			RN	[3]
OC	NOBI_TAXID=7227;			RP	SEQUENCE FROM N.A.
RN	[1] MEDLINE=2015606; PubMed=10731132;			RX	Medline=22426070; PubMed=12537573;
RP	SEQUENCE FROM N.A.			RA	Kaninker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA	Asburner M., Celniker S.E.,			RA	"the transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomic perspective,"
RT	"The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomic perspective,"			RN	Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RT	a genomic perspective,"			RA	[4]
RT	"The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomic perspective,"			RA	Medline=22426069; PubMed=12537572;
RT	"The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomic perspective,"			RA	Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RT	"The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomic perspective,"			RA	Bradecy P., Huang Y., Kaninker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Hebburner M., Gelbart W.M., Rubin G.M., Lewis S.B., Lewis S.B.,
RT	"annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a systematic review,"			RA	Noobi T., Adams M.D., Celiker S.B., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celiker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RT	"annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a systematic review,"			RP	Medline=2015606; PubMed=10731132;
RP	SEQUENCE FROM N.A.			RN	Sequence 1;
RP	SEQUENCE FROM N.A.			RP	Sequence 2;
RP	SEQUENCE FROM N.A.			RN	Sequence 3;



[1]

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K10;  
 ID L.J., Bannantine J., Zhang Q., Amosin A., Alt D., Kapur V.;  
 AC submitted (SRR2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE017233; ASN04008.1; -.  
 KW Hypothetical protein.

SQ SEQUENCER 227 AA; 24027 MW; 952EA4962C0EB199 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 227;  
 Best Local Similarity 70.0%; Pred. No. 1.3e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LKAMDPTPPL 10  
 Db 146 LAAQDPPL 155

RESULT 12  
 Q96ID3 PRELIMINARY; PRT; 243 AA.  
 ID Q96ID3,  
 AC 096ID3;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DB KIAA115 protein (Fragment).  
 GN Name=KIAA115,  
 OS Homo sapiens (Human).  
 OC Burkhardt, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22308257; PubMed=12477932;  
 RA Strausberg R.L., Feingold B.A., Grouse I.H., Derge J.G.,  
 RA Klausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Butetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore S.I., Wang J., Heleb F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Usdin T.B., Tothilak S., Carninci P., Prange C.,  
 RA Raha S.S., Loqueilano N.A., Peters G.J., Abramson R.D., Mulally S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Rahey J., Helton B., Kettenbach M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schniech A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL [2]  
 RN SEQUENCER FROM N.A.  
 RC TISSUE=Placenta;  
 RA Strausberg R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC007629; AAH07629.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 243 AA; 24559 MW; 9094604DB4A93228 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 243;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LKAMDPTPPL 9  
 Db 130 LRSQDPTPP 138

RESULT 13  
 Q9G1P6\_ PRELIMINARY; PRT; 268 AA.  
 ID Q9G1P6;  
 AC 06G1P6;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DR 1-acyl-sn-glycerol-3-phosphate acyltransferase.  
 DE Name=pIBC; Order=LocusName=BIL6290;  
 OS Bartonella henselae (Rochalimaea henselae).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bartonellaceae; Bartonella.  
 OX NCBI\_TaxID=38323;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 49882 / Houston 1;  
 RX PubMed=15210978;  
 RA Alsmark U.C.M., Frank A.C., Karlberg B.O., Legault B.-A., Ardell D.H.,  
 RA Canback B., Eriksson A.-S., Naelund A.K., Handley S.A., Huovit M.,  
 RA La Scola B., Holmberg M., Andersson S.G.B.;  
 RT "The louse-borne human pathogen Bartonella quintana is a genomic  
 derivative of the zoonotic agent Bartonella henselae.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).  
 DR EMBL; BX89599; CAR2391.1; -.  
 DR InterPro; IPR001223; Acyltransferase.  
 DR Pfam; PF0153; Acyltransferase; 1.  
 DR SMART; SM00563; P1SC; 1.  
 DR SMART; SM00563; P1SC; 1.  
 KW Acyltransferase; Complete proteome; Transferase.  
 SQ SEQUENCER 268 AA; 30957 MW; 2F95B7EEFBDB8B55 CRC64;

Query Match 72.2%; Score 39; DB 2; Length 268;  
 Best Local Similarity 77.8%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LKAMDPTPPL 9  
 Db 240 LAAQDPPL 248

RESULT 14  
 Q9V3M1 PRELIMINARY; PRT; 320 AA.  
 ID Q9V3M1  
 AC 06V3M1;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE SPV074 DNA topoisomerase.  
 GN Name=SPV074;  
 OS Smallpox virus (SPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC SV40 virus;  
 OX NCBI\_TaxID=10276;  
 RN [1]  
 RP SEQUENCER FROM N.A.  
 RX MEDLINE=21634277; PubMed=11752168;  
 RA Alonso C.L., Turner E.R., Lu Z., Zbak L., Osorio F.A., Balinsky C.,  
 RA Kutish G.F., Rock D.L.;  
 RT "The genome of smallpox virus.";  
 RL J. Virol. 76:783-790(2002);  
 DR AP410153; AAL6813.1; -.  
 DR IISPP; P08585; 1NCB.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0003917; F:DNA topoisomerase type I activity; IEA.  
 DR GO; GO:0016853; F:isomerase activity; IEA.  
 DR GO; GO:000265; P:DNA topological change; IEA.  
 DR GO; GO:000268; P:DNA unwinding; IEA.  
 DR InterPro; IPR01010; DNA\_brk\_join\_enz.  
 DR InterPro; IPR001631; Topoisomerase\_I.  
 DR Pfam; PF01028; Topoisom\_I\_1.  
 DR PRINTS; PR00416; BUTERMASBE.  
 DR PROSITE; PS00176; TOPOISOMERASE\_I\_EUK; UNKNOWN\_1.  
 KW Isomerase.

SQ SEQUENCE 320 AA; 38179 MW; 97F9B9442DD1DC5 CRC64;

Query Match 72.2%; Score 39; DB 2; length 320;  
 Best Local Similarity 50.0%; Pred. No. 2e+02; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 4; MisMatches 1; Indels 0; Gaps 0;

Qy	1	1	1	1	1	1	1
Db	241	IKS1DPPVPPi	250				

**RESULT 15**

O9K437	PRELIMINARY;	PRT;	693 AA.
ID	O9K437;		
AC	O9K437;		
DT	01-OCT-2000 (TREMBirel. 15; Last sequence update)		
DT	01-MAR-2004 (TREMBirel. 26; Last annotation update)		
DB	putative hydrolase.		
GN	Orderedlocusnames=SCO162; ORFNames=SC022.08c;		
OS	Streptomyces coelicolor.		
OC	Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;		
OC	Streptomycineae; Streptomycetaceae; Streptomyces.		
OX	NCBI_TaxID=1902;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SRAINS-A3(2) / MI45;		
RX	MEDLINE=21986410; PubMed=12000953; DOI=10.1038/417141a;		
RA	Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,		
RA	Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,		
RA	Harper D., Bateman A., Brown S., Chanda G., Chen C.W., Collins M.,		
RA	Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,		
RA	Huang C.-H., Kiese T., Larke L., Murphy L.D., Oliver K., O'Neill S.,		
RA	Rabinowitzsch E., Rajandream M.A., Rutherford K.M., Rutter S.,		
RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,		
RA	Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J.,		
RA	Hopwood D.A.;		
RT	"Complete genome sequence of the model actinomycete Streptomyces		
RT	coelicolor A3(2)",		
RL	Nature 417:141-147(2002).		
DR	EMBL; AL939107; CAB95281.1; -.		
DR	GO: GO-0016787; FHydrolyase activity; Hydrolyzing O-glycosyl . . . ; IEA.		
DR	GO: GO-004553; FHydrolyase activity; Hydrolyzing O-glycosyl . . . ; IEA.		
DR	GO: GO-005975; Pcarbohydrate metabolism; IEA.		
DR	InterPro; IPR00879; Gal_bind like.		
DR	InterPro; IPR06101; Glyco_Hydro_2.		
DR	InterPro; IPR006102; Glyco_hydro_2IG.		
DR	InterPro; IPR006104; Glyco_hydro_2SB.		
DR	InterPro; IPR006103; Glyco_Hydro_2TIM.		
DR	InterPro; IPR002088; PPA.		
DR	Pfam; PF00703; Glyco_hydro_2; 1.		
DR	Pfam; PF02836; Glyco_hydro_C; 1.		
DR	Pfam; PF02837; Glyco_hydro_2_N; 1.		
DR	PRINTS; PR00132; GLYHYDRASE2.		
DR	PROSITE; PS00904; PPTA, UNKNOWN_1.		
KW	complete proteome; Hydrolase.		
SQ	SEQENCE 693 AA; 75941 MW; E54676BCCA33A921 CRC64;		

Query Match 72.2%; Score 39; DB 2; length 693;  
 Best Local Similarity 70.0%; Pred. No. 4.6e+02; Mismatches 1; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; MisMatches 1; Indels 0; Gaps 0;

Qy	1	1	1	1	1	1	1
Db	420	IKALDPPTRPV	429				

Search completed: January 6, 2005, 10:17:43  
 Job time : 90.6757 secs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: January 6, 2005, 10:08:37 ; Search time 79,4595 seconds  
(without alignments)  
45.146 Million cell updates/sec

Title: US-10-047-945-1  
Perfect score: 54  
Sequence: 1 LKAMDPPTPL 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries  
Database :

- 1: geneseq\_23Sep04;\*
- 2: geneseqD19808;\*
- 3: geneseqD20008;\*
- 4: geneseqD20018;\*
- 5: geneseqD20028;\*
- 6: geneseqD2003a;\*
- 7: geneseqD2003b;\*
- 8: geneseqD2004a;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 1s derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	54	100.0	10	2 AAW53843	Aaw53843 N-terminal
2	54	100.0	10	7 ABB80222	Abb80222 Synthetic
3	54	100.0	11	7 ABB80226	Abb80226 Synthetic
4	54	100.0	12	7 ABB80225	Abb80225 Synthetic
5	54	100.0	15	2 AAW11575	Aaw11575 N-terminal
6	54	100.0	15	2 AAW53841	Aaw53841 N-terminal
7	54	100.0	15	7 ABB80223	Abb80223 Synthetic
8	50	92.6	9	7 ABB80227	Abb80227 Synthetic
9	43	79.6	8	7 ABB80228	Abb80228 Synthetic
10	42	77.8	94	4 AAC002179	Aac002179 Human pol
11	41	75.9	165	4 ABB8900	Abb8900 Drosophila
12	39	72.2	459	3 AAB59012	Aab59012 Breast milk
13	38	70.4	78	4 AAM85892	Aam85892 Human imm
14	38	70.4	108	7 ABM4107	Abm74107 DNA clone
15	38	70.4	2	2 AAY1943	Aay1943 Yeast pro
16	38	70.4	349	3 AAGJ7097	Aagj7097 Arabidops
17	38	70.4	349	3 AAG47069	Aag47069 Arabidops
18	38	70.4	369	3 AAG24233	Aag24233 Arabidops
19	38	70.4	369	5 ABB53666	Abb53666 Herbicida
20	38	70.4	405	3 AAG47028	Aag47028 Arabidops
21	37	68.5	15	2 AAW39043	Aaw39043 Peptidex
22	37	68.5	210	2 RAY00125	Aay00125 Enterococ
23	37	68.5	210	5 ABP03344	Abp03344 E faecali
24	37	68.5	210	6 ABU88372	Abu88372 E. faecal
25	37	68.5	210	6 ABU13623	Abu13623 Enterococ

Post-processing: Minimum Match 0%  
Maximum Match 100%

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Post-processing: Minimum Match 0%  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

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Maximum Match 100%

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Post-processing: Minimum Match 0%  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

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Post-processing: Minimum Match 0%  
Maximum Match 100%

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- 8: geneseqD2004a;\*

Post-processing: Minimum Match 0%  
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- 8: geneseqD2004a;\*

Post-processing: Minimum Match 0%  
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Maximum Match 100%

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- 4: geneseqD20018;\*
- 5: geneseqD20028;\*
- 6: geneseqD2003a;\*
- 7: geneseqD2003b;\*
- 8: geneseqD2004a;\*

CC snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity to horse proteins  
 CC  
 XX Sequence 10 AA;  
 SQ Query Match 100.0%; Score 54; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.031; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKAMDTPPL 10  
 Db 1 ||||||| 10

RESULT 2  
 ABB80222  
 ID ABB80222 standard; peptide; 10 AA.  
 AC XX  
 AC XX  
 AC ABB80222;  
 DT 06-NOV-2003 (first entry)  
 XX Synthetic LTNF, LT-10.  
 DB XX  
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.  
 KW XX  
 OS Synthetic.  
 PN XX  
 OS WO2003060471-A2.  
 PN XX  
 PD XX  
 PR XX  
 PR 14-JAN-2003; 2003WO-US001044.  
 XX PR 14-JAN-2002; 2002US-00047945.  
 PA XX  
 PA (LIPPS/) LIPPS B V.  
 PA (LIPPS/) LIPPS F W.  
 PI XX  
 PI Lipps BV, Lipps FW;  
 PA XX  
 DR XX  
 PT XX  
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.  
 PT XX  
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.  
 PT XX  
 PS XX  
 PS Claim 7; Page 3; 24pp; English.

XX The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA

XX Sequence 10 AA;  
 SQ Query Match 100.0%; Score 54; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.031; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKAMDTPPL 10  
 Db 1 ||||||| 10

RESULT 3  
 ABB80226  
 ID ABB80226 standard; peptide; 11 AA.  
 AC XX  
 AC ABB80226;  
 DT 06-NOV-2003 (first entry)  
 DE Synthetic LTNF, LT-11.  
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; Systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.  
 KW XX  
 OS Synthetic.  
 PN XX  
 PN WO2003060471-A2.  
 PN XX  
 PD XX  
 PR XX  
 PR 14-JAN-2003; 2003WO-US001044.  
 XX PR 14-JAN-2002; 2002US-00047945.  
 PA XX  
 PA (LIPPS/) LIPPS B V.  
 PA (LIPPS/) LIPPS F W.  
 PI XX  
 PI Lipps BV, Lipps FW;  
 PA XX  
 DR XX  
 PT WPI; 2003-636703/60.  
 PT XX  
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.  
 PT XX  
 PS XX  
 PS Claim 7; Page 4; 24pp; English.

CC The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA

SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.034; Mismatches 0; Indels 0; Gaps 0;

Qy

1 LKAMDPTPPL 10

Db 1 LKAMDPTPPL 10

RESULT 4

ABB80225 standard; peptide; 12 AA.

ABB80225; (first entry)

XX DT 06-NOV-2003

XX DB Synthetic LTNF, LT-12.

XX KW lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; Systemic Lupus Erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.

OS Synthetec.

OS XX PN WO2003060471-A2.

XX PD 24-JUL-2003.

XX PR 14-JAN-2003; 2003WO-US001044.

XX PR 14-JAN-2002; 2002US5-00047945.

XX PA (LIPPS/) LIPPS B V.

XX PA (LIPPS/) LIPPS F W.

XX PI LIPPS FW, LIPPS BV;

XX DR WPI; 1997-011287/01.

XX PT Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal peptide.

XX PS Claim 7, Col 9; 9pp; English.

XX CC The present sequence is from the N-terminus of a 68 kD protein purified

CC from the serum of the opossum *Didelphis virginiana*. The full-length

CC protein is a lethal toxin neutralising factor (LTNF). The use of Purified

CC LTNF or of the chemically synthesised 15mer N-terminal peptide for

CC treating victims of bee stings, scorpion stings and bacterial or plant

CC toxins is claimed. The patent disclosure does not provide any evidence

CC for neutralising activity against these various toxins. There is evidence

CC of significant neutralising activity of the opossum LTNF and the 15mer

CC peptide against venom from snakes of the families Crotalidae, Elapidae,

CC Hydrophiidae and Viperidae. (Updated on 25-MAR-2003 to correct PP field.)

XX SQ Sequence 15 AA;

SQ Query Match 100.0%; Score 54; DB 2; Length 15;

SQ Best Local Similarity 100.0%; Pred. No. 0.047; Mismatches 0; Indels 0; Gaps 0;

SQ Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

AAW1575 standard; peptide; 15 AA.

AAW1575; (revised)

XX DT 25-MAR-2003

XX DB N-terminal peptide from lethal toxin neutralising factor.

XX KW Lethal toxin neutralising factor; LTNF; opossum; bee toxin; snake bite; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.

XX OS Didelphis virginiana.

XX PN US5576297-A.

XX PD 19-NOV-1996.

XX PR 22-SEP-1994; 94US-00310340.

XX PR 10-MAY-1993; 93US-00058387.

XX PA (LIPPS/) LIPPS B V.

XX PA (LIPPS/) LIPPS F W.

XX PI LIPPS FW, LIPPS BV;

XX DR WPI; 1997-011287/01.

XX PT Treatment of victims of bee or scorpion stings or plant or bacterial

PT toxins - by admin. of lethal toxin-neutralising factor or its N-terminal

PT peptide.

XX PS Claim 7, Col 9; 9pp; English.

XX CC The present sequence is from the N-terminus of a 68 kD protein purified

CC from the serum of the opossum *Didelphis virginiana*. The full-length

CC protein is a lethal toxin neutralising factor (LTNF). The use of Purified

CC LTNF or of the chemically synthesised 15mer N-terminal peptide for

CC treating victims of bee stings, scorpion stings and bacterial or plant

CC toxins is claimed. The patent disclosure does not provide any evidence

CC for neutralising activity against these various toxins. There is evidence

CC of significant neutralising activity of the opossum LTNF and the 15mer

CC peptide against venom from snakes of the families Crotalidae, Elapidae,

CC Hydrophiidae and Viperidae. (Updated on 25-MAR-2003 to correct PP field.)

XX SQ Sequence 15 AA;

SQ Query Match 100.0%; Score 54; DB 7; Length 12;

SQ Best Local Similarity 100.0%; Pred. No. 0.038; Mismatches 0; Indels 0; Gaps 0;

SQ Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ ID AAW53841 standard; peptide; 15 AA.

SQ AC AAW53841;

SQ DT 08-JUL-1998 (first entry)

Query Match 100.0%; Score 54; DB 7; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.038; Mismatches 0; Indels 0; Gaps 0;

Qy

1 LKAMDPTPPL 10

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 54; DB 7; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.038; Mismatches 0; Indels 0; Gaps 0;

Qy

1 LKAMDPTPPL 10

XX SQ Sequence 12 AA;





XX Tang YT, Liu C, Dumanac RT;  
 XX WPI; 2001-514838/56.  
 DR N-PSDB; AAI82110.  
 XX PT Isolated nucleic acids and polypeptide, useful for preventing, diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.  
 XX Claim 20; SEQ ID NO 16071; 1399pp + Sequence Listing; English.  
 XX CC The invention relates to human polynucleotides (AA179341-AA193841) and  
 CC the encoded proteins (AA00010-AA03910) that exhibit activity relating to  
 cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 e.g., stem cell growth factor activity, haemopoiesis regulating  
 activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note, the sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at [ftp://ftp.wipo.int/pub/published\\_pct\\_sequences](ftp://ftp.wipo.int/pub/published_pct_sequences)  
 XX SQ Sequence 94 AA:

Query	Match	Score	DB	Length
Best Local Matches	Similarity 77.8%; Conservative 7;	42; Pred. No. 27;	94;	
QY	1 LKAMDPTPP 9	1; Mismatches 0;	Indels 0;	Gaps 0;
Db	48 LKSQDPTPP 56			

RESULT 12  
 ID AAB59012  
 XX AAB59012 standard; protein; 459 AA.  
 AC AAB59012;  
 XX DT 27-MAR-2001 (first entry)  
 DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 720.  
 XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
 KW nootropic; neuroprotective; antiviral; anti-allergic; hepatotoxic;  
 KW antidiabetic; anti-inflammatory; antiulcer; vulnerary; anticonvulsant;  
 KW antibacterial; antifungal; antiparasitic; cardiotonic; immune disorder;  
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
 KW cardiovascular disorder; wound healing; neurological disease.  
 OS Homo sapiens.  
 XX PN WO200055173-A1.  
 XX PD 21-SEP-2000.  
 XX PP 08-MAR-2000; 2000WO-US005881.  
 PR 12-MAR-1999; 99US-0124270P.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Ruben SM;  
 XX DR WPI; 2000-611515/58.  
 XX DR N-PSDB; AAF21915.  
 XX PT New human breast and ovarian cancer associated gene sequences and the  
 PT polypeptides encoded by these genes, useful in the prevention, treatment  
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and  
 PT neurological diseases.  
 XX PS Claim 11; Page 1174-1176; 1299pp; English.  
 XX CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
 CC proteins AAB5811 - AAB59128. The DNA and protein sequences are  
 CC associated with breast and ovarian cancer. Included in the invention are  
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
 PT isolation and characterisation of the DNA and protein sequences of the  
 CC invention. The breast and ovarian cancer associated DNA protein, agonist  
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;  
 CC neuroprotective; antiviral; antiallergic; hepatotoxic; antidiabetic;

ABB58900  
 ID ABB58900 standard; protein; 165 AA.  
 AC ABB58900;  
 XX DT 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster polypeptide SEQ ID NO 3492.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX OS Drosophila melanogaster.  
 XX WO200171042-A2.

XX PT 27-SEP-2001.  
 XX PR 23-MAR-2001; 2001WO-US009231.  
 XX PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX PA (PEKB ) PE CORP NY.  
 XX PT Venter JC, Adams M, Li PWD, Myers EW;  
 DR WPI; 2001-655660/75.  
 DR N-PSDB; ABL03003.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX Disclosure; SEQ ID NO 3492; 21pp + Sequence Listing; English.

CC	antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and carciotic activity. The polynucleotide and protein sequences are used in the diagnosis of cancer particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and antagonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmunity, haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemia; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and infectious diseases	CC	14-AUG-2000; 2000US-0225759P.
CC	Sequence 459 AA;	SQ	18-AUG-2000; 2000US-0226778P.
CC	Query Match 72 %; Score 39; DB 3 ; Length 459; Best Local Similarity 66.7%; Pred. No. 4.1e+02; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	QY	22-AUG-2000; 2000US-0226681P.
CC	1 LKAMDPPTPP 9  ::        Db 346 LRSQDPTPP 354	DB	22-AUG-2000; 2000US-0226869P.
XX	RESULT 13	PR	23-AUG-2000; 2000US-0227118P.
XX	AAMB5892 standard; protein; 78 AA.	PR	30-AUG-2000; 2000US-0228924P.
XX	AAMB5892;	PR	01-SEP-2000; 2000US-0229281P.
XX	07-NOV-2001 (first entry)	PR	01-SEP-2000; 2000US-0229344P.
XX	DT Human immune/haematopoietic antigen SEQ ID NO:13485.	PR	01-SEP-2000; 2000US-0229345P.
XX	KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cycostatic; gene therapy; vaccine; metastasis.	PR	05-SEP-2000; 2000US-0229509P.
XX	OS Homo sapiens.	PR	05-SEP-2000; 2000US-0229513P.
XX	WO201517182-A2.	PR	06-SEP-2000; 2000US-0230437P.
XX	PN	PR	08-SEP-2000; 2000US-0231242P.
XX	PD 09-AUG-2001.	PR	01-SEP-2000; 2000US-0231243P.
XX	PF 17-JAN-2001; 2001WO-US001354.	PR	01-SEP-2000; 2000US-0231244P.
PR	31-JAN-2000; 2000US-0179065P.	PR	03-SEP-2000; 2000US-0231245P.
PR	04-FEB-2000; 2000US-0180028P.	PR	08-SEP-2000; 2000US-0231249P.
PR	24-FEB-2000; 2000US-0184664P.	PR	01-SEP-2000; 2000US-0231250P.
PR	02-MAR-2000; 2000US-018350P.	PR	01-SEP-2000; 2000US-0231253P.
PR	16-MAR-2000; 2000US-0189074P.	PR	14-SEP-2000; 2000US-0233064P.
PR	17-MAR-2000; 2000US-0190076P.	PR	14-SEP-2000; 2000US-0233238P.
PR	18-APR-2000; 2000US-018123P.	PR	14-SEP-2000; 2000US-0233414P.
PR	19-MAY-2000; 2000US-020515P.	PR	14-SEP-2000; 2000US-0233438P.
PR	07-JUN-2000; 2000US-0209467P.	PR	14-SEP-2000; 2000US-0233480P.
PR	28-JUN-2000; 2000US-0214886P.	PR	14-SEP-2000; 2000US-0233484P.
PR	30-JUN-2000; 2000US-0215135P.	PR	14-SEP-2000; 2000US-0233488P.
PR	07-JUL-2000; 2000US-0216547P.	PR	14-SEP-2000; 2000US-0233492P.
PR	07-JUL-2000; 2000US-0216880P.	PR	14-SEP-2000; 2000US-0233496P.
PR	11-JUL-2000; 2000US-0217487P.	PR	14-SEP-2000; 2000US-0233500P.
PR	14-JUL-2000; 2000US-0218290P.	PR	14-SEP-2000; 2000US-0233504P.
PR	14-JUL-2000; 2000US-0220563P.	PR	14-SEP-2000; 2000US-0233508P.
PR	26-JUL-2000; 2000US-0220564P.	PR	14-SEP-2000; 2000US-0233512P.
PR	14-AUG-2000; 2000US-0224518P.	PR	14-SEP-2000; 2000US-0233516P.
PR	14-AUG-2000; 2000US-0224519P.	PR	14-SEP-2000; 2000US-0233520P.
PR	14-AUG-2000; 2000US-0225213P.	PR	14-SEP-2000; 2000US-0233524P.
PR	14-AUG-2000; 2000US-0225149P.	PR	14-SEP-2000; 2000US-0233528P.
PR	14-AUG-2000; 2000US-0225266P.	PR	14-SEP-2000; 2000US-0233532P.
PR	14-AUG-2000; 2000US-0225367P.	PR	14-SEP-2000; 2000US-0233536P.
PR	14-AUG-2000; 2000US-022568P.	PR	14-SEP-2000; 2000US-0233540P.
PR	14-AUG-2000; 2000US-0225210P.	PR	14-SEP-2000; 2000US-0233544P.
PR	14-AUG-2000; 2000US-0225547P.	PR	14-SEP-2000; 2000US-0233548P.
PR	14-AUG-2000; 2000US-022557P.	PR	14-SEP-2000; 2000US-0233552P.
PR	14-AUG-2000; 2000US-0225758P.	PR	14-SEP-2000; 2000US-0233556P.

		Db	5 LPALPFPPL 14
<b>RESULT 14</b>			
PR	08-NOV-2000; 20001SS-0246611P.		
PR	08-NOV-2000; 20001SS-0246613P.		
PR	17-NOV-2000; 20001SS-0249207P.		
PR	17-NOV-2000; 20001SS-0249208P.		
PR	17-NOV-2000; 20001SS-0249210P.		
PR	17-NOV-2000; 20001SS-0249211P.		
PR	17-NOV-2000; 20001SS-0249212P.		
PR	17-NOV-2000; 20001SS-0249213P.		
PR	17-NOV-2000; 20001SS-0249214P.		
PR	17-NOV-2000; 20001SS-0249215P.		
PR	17-NOV-2000; 20001SS-0249216P.		
PR	17-NOV-2000; 20001SS-0249217P.		
PR	17-NOV-2000; 20001SS-0249218P.		
PR	17-NOV-2000; 20001SS-0249244P.		
PR	17-NOV-2000; 20001SS-024925P.		
PR	17-NOV-2000; 20001SS-0249264P.		
PR	17-NOV-2000; 20001SS-0249265P.		
PR	17-NOV-2000; 20001SS-024927P.		
PR	17-NOV-2000; 20001SS-0249299P.		
PR	17-NOV-2000; 20001SS-0249300P.		
PR	01-DEC-2000; 20001SS-0250160P.		
PR	01-DEC-2000; 20001SS-0250391P.		
PR	05-DEC-2000; 20001SS-0251030P.		
PR	05-DEC-2000; 20001SS-0251988P.		
PR	05-DEC-2000; 20001SS-0256719P.		
PR	06-DEC-2000; 20001SS-0251479P.		
PR	08-DEC-2000; 20001SS-0251556P.		
PR	08-DEC-2000; 20001SS-0251868P.		
PR	08-DEC-2000; 20001SS-0251869P.		
PR	08-DEC-2000; 20001SS-0251989P.		
PR	08-DEC-2000; 20001SS-0251990P.		
PR	11-DEC-2000; 20001SS-0254097P.		
PR	05-JAN-2001; 20011SS-0259678P.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
PA	PT Rosen CH, Barash SC, Ruben SM;		
XX	XX		
DR	WPI: 2001-493426/52.		
DR	N-PSDB; AAK5673.		
XX	PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.		
XX	XX		
PS	Claim 11; SEQ ID NO 13485; 3071pp + sequence Listing; English.		
XX	XX		
CC	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM02170 to AAM9191. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haemopoietic-derived cells. AAK64703 to AAK7694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK5492 to AAK4950 and AAM82169 represent sequences used in the exemplification of the present invention		
CC	Sequence 78 AA;		
SQ	Sequence 108 AA;		
XX	Query Match 70.4%; Score 38; DB 4; length 78; Best Local Similarity 70.0%; Pred. No. 1e+02; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		
QY	1 LKAMDTPPL 10		
<b>RESULT 15</b>			
AAV3943	Query Match 70.4%; Score 38; DB 7; Length 108;		
ID AAV3943	Best Local Similarity 75.0%; Pred. No. 1.e+02;		
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
AC AAV3943;			
XX DT 21-DEC-1999 (first entry)			

DB Yeast protein kinase #10.

XX Prediction; secondary structure; alignment; evolutionary conservation;

KW homology; periodicity; co-variation analysis; antigenic site;

KW site directed mutagenesis; interaction.

XX Saccharomyces cerevisiae.

OS US5958784-A.

XX PN

PD 28-SEP-1999.

XX PP 25-MAR-1992; 92US-00857224.

XX PR 25-MAR-1992; 92US-00857224.

XX PA (BENN/)

XX PI BENNER S A.

XX DR

XX WPI; 1999-570766/4B.

XX PT Predicting the folded structure of proteins.

XX PS Disclosure; Col 225-228; 113pp; English.

PS

CC Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure. Active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges. Active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as the guides for site directed mutagenesis studies, and for understanding the interaction of a protein with other molecules

SQ Sequence 267 AA;

Query Match 70.4%; Score 38; DB 2; Length 267;  
Best Local Similarity 70.0%; Pred. No. 3.5e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	LKAMDPPTPL	10
	:		
Db	31	LKVVDPTPL	40

Search completed: January 6, 2005, 10:22:43  
Job time : 83.4595 sec

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On protein - protein search, using SW model

Run on: January 6, 2005, 10:23:04 ; search time 67.5676 Seconds  
(without alignment) ; 53.365 Million cell updates/sec

Title: US-10-047-945-1  
Perfect score: 54.  
Sequence: 1 LKAMDPTPPL 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgmn\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep:  
2: /cgmn\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep:  
3: /cgmn\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pep:  
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7: /cgmn\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep:  
8: /cgmn\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep:  
9: /cgmn\_6/ptodata/1/pubaa/US09\_PUBCOMB.pep:  
10: /cgmn\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep:  
11: /cgmn\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep:  
12: /cgmn\_6/ptodata/1/pubaa/US09C\_NEW\_PUB.pep:  
13: /cgmn\_6/ptodata/1/pubaa/US10\_PUBCOMB.pep:  
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15: /cgmn\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pep:  
16: /cgmn\_6/ptodata/1/pubaa/US10D\_PUBCOMB.pep:  
17: /cgmn\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep:  
18: /cgmn\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pep:  
19: /cgmn\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep:  
20: /cgmn\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	54	100.0	10	14	US-10-047-945-1
2	54	100.0	11	14	US-10-047-945-5
3	54	100.0	12	14	US-10-047-945-4
4	54	100.0	15	14	US-10-047-945-2
5	50	92.6	9	14	US-10-047-945-6
6	43	79.6	8	14	US-10-047-945-7
7	41	75.9	80	15	US-10-047-599-253125
8	41	75.9	148	16	US-10-047-963-133345
9	40	74.1	153	17	US-10-047-25326
10	39	72.2	137	17	US-10-047-115-27629
11	39	72.2	169	16	US-10-047-963-162813
12	39	72.2	205	16	US-10-047-963-162816
13	39	72.2	459	9	US-09-925-298-720

RESULT 1  
US-10-047-945-1  
; Sequence 1, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION;  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENT FOR IMMUNOGLOBULIN B  
; TITLE OF INVENTION: (19E) IMPLICATED DISORDERS  
; FILE REFERENCE: FILPAT015US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM  
; OTHER INFORMATION: US 5,576,297.  
US-10-047-945-1  
Query Match 100.0%; Score 54; DB 14; length 10;  
Best Local Similarity 100.0%; Pred. No. 0.065; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0;  
Qy 1 LKAMDPTPPL 10  
Db 1 LKAMDPTPPL 10

**RESULT 2**  
US-10-047-945-5  
; Sequence 5, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BONIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS  
; FILE REFERENCE: FWLPA101S  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIORITY NUMBER: US/10/047,945  
; SEQ ID NO 5 ID NOS: 7  
; PRIORITY FILING DATE:  
; PRIORITY NUMBER:  
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS  
; SEQ ID NO 5 LENGTH: 11  
; TYPE: PRT  
; LENGTH: 11  
; NAME/KEY:  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-11 of 2 above.

**RESULT 3**  
US-10-047-945-4  
; Sequence 4, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BONIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS  
; FILE REFERENCE: FWLPA101S  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIORITY NUMBER:  
; PRIORITY FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS  
; SEQ ID NO 4 LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; FEATURE:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.

**RESULT 4**  
US-10-047-945-4  
; Sequence 4, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
Query Match 100.0%; Score 54; DB 14; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.078; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LKAMDPTEPL 10  
Db 1 LKAMDPTEPL 10

**RESULT 5**  
US-10-047-945-6  
; Sequence 6, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BONIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; TITLE OF INVENTION: (IGE) IMPLICATED DISORDERS  
; FILE REFERENCE: FWLPA101S  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIORITY NUMBER:  
; PRIORITY FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS  
; SEQ ID NO 6 LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.

**RESULT 6**  
US-10-047-945-7  
; Sequence 7, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
Query Match 92.6%; Score 50; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LKAMDPTEP 9  
Db 1 LKAMDPTEP 9

```

; APPLICANT: LIPPS, BINNIE V.
; APPLICANT: LIPPS, FREDERICK W.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E
; TITLE OF INVENTION: (15B) IMPLICATED DISORDERS
; FILE REFERENCE: FMPAT015US
; CURRENT APPLICATION NUMBER: US/10/047,945
; CURRENT FILING DATE: 2002-01-14
; PRIORITY FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO: 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above.
; US-10-047-945-7

Query Match 79.6%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKAMDPTP 8
Db 1 LKAMDPTP 8

RESULT 7
US-10-424-599-253125
; Sequence 253125, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 253125
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35767C.1.pep
; US-10-424-599-253125

Query Match 79.6%; Score 43; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 51; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LKAMDPTP 10
Db 62 LKAMDPTP 71

RESULT 8
US-10-437-963-133945
; Sequence 133945, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

Query Match 79.5%; Score 41; DB 15; Length 80;
Best Local Similarity 70.0%; Pred. No. 51; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LKAMDPTP 10
Db 62 LKAMDPTP 71

RESULT 9
US-10-425-115-235826
; Sequence 235826, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 235826
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(153)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_146658C.1.pep
; US-10-425-115-235826

Query Match 74.1%; Score 40; DB 17; Length 153;
Best Local Similarity 70.0%; Pred. No. 1.4e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LKAMDPPPL 10
Db 62 LSALDPPPL 71

RESULT 10
US-10-425-115-276822
; Sequence 276822, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.


```

Query Match      Score 39; DB 17; Length 137;  
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 AMDPTPPL 10  
 Db      125 AMDPPPL 132

---

RESULT 11  
 US-10-437-963-162813  
 ; Sequence 162813, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovacic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21-(5321)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 162813  
 ; LENGTH: 169

Query Match      Score 39; DB 17; Length 137;  
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 AMDPTPPL 10  
 Db      125 AMDPPPL 132

---

RESULT 12  
 US-10-437-963-162816  
 ; Sequence 162816, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovacic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei

Query Match      Score 39; DB 17; Length 137;  
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 AMDPTPPL 10  
 Db      125 AMDPPPL 132

---

RESULT 13  
 US-03-921-298-720  
 ; Sequence 720, Application US/09925298  
 ; Publication No. US20020039764A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA103  
 ; CURRENT APPLICATION NUMBER: US/09/925,298  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05881  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 01/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 846  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 720  
 ; LENGTH: 459  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (50)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Query Match      Score 39; DB 16; Length 169;  
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LKAMDPTPPL 10  
 Db      61 LSSLDPSPL 70

---

RESULT 14  
 US-10-102-806-720  
 ; Sequence 720, Application US/10102806  
 ; Publication No. US20030054421A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

```

; FILE REFERENCE: PA103P1CL
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 720
LENGTH: 459
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (50)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-720

Query Match          72.2%; Score 39; DB 14; Length 459;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches   6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy      1 LKAMDPTPP 9
Db      346 LRSDODPTPP 354

RESULT 15
US-10-767-701-51220
; Sequence 51220, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21 (5535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 51220
; LENGTH: 75

; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3481-060-Q6-K1-D12.pep
US-10-767-701-51220

Query Match          70.4%; Score 38; DB 16; Length 75;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches   7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1 LKAMDPTPP 9
Db      2 LKAMDPPPP 10

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Search completed: January 6, 2005, 10:44:42  
 Job time : 68.5676 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 6, 2005, 10:09:51 ; Search time 20.2703 Seconds  
 (without alignment)  
 32.717 Million cell updates/sec

Title:	US-10-047-945-1
Perfect Score:	54
Sequence:	LIPKMDPTPL 10
Scoring table:	BLOSUM62
Gapop:	10.0 , Gapext 0.5
Searched:	478139 seqs, 63318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/pctdata/1/iaaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/pctdata/1/iaaa/6A\_COMB.pep:\*
- 3: /cgn2\_6/pctdata/1/iaa/6B\_COMB.pep:\*
- 4: /cgn2\_6/pctdata/1/iaa/PCTUS\_Comb.pep:\*
- 5: /cgn2\_6/pctdata/1/iaa/backfiles1.pep:\*
- 6: /cgn2\_6/pctdata/1/iaa/backfiles1.pep:\*

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	54	100.0	10	1 US-08-657-163A-2
2	54	100.0	15	1 US-08-310-340A-1
3	54	100.0	15	1 US-08-657-163A-1
4	41	75.9	253	4 US-09-270-767-43223
5	38	70.4	267	42 US-07-857-2248-42
6	37	68.5	15	3 US-08-602-999A-444
7	37	68.5	15	4 US-09-500-124-444
8	37	68.5	210	4 US-09-071-035-232
9	37	68.5	256	4 US-09-071-035-230
10	37	68.5	291	4 US-09-134-000-6676
11	37	68.5	306	4 US-09-134-000-6676
12	36	66.7	323	4 US-09-489-039A-13655
13	36	66.7	338	4 US-09-248-796A-20624
14	35	64.8	27	4 US-09-270-767-57016
15	35	64.8	206	4 US-09-530-092-166
16	35	64.8	315	1 US-08-571-758-12
17	35	64.8	315	1 US-08-903-984A-12
18	35	64.8	315	1 US-08-903-983-12
19	35	64.8	323	4 US-09-249-796A-16328
20	35	64.8	346	1 US-08-185-151-2
21	35	64.8	405	4 US-09-489-039A-9126
22	35	64.8	648	1 US-08-185-282-1
24	35	64.8	648	1 US-08-185-282-2
25	35	64.8	648	1 US-08-185-282-3
27	35	64.8	648	1 US-08-185-282-4
35	64.8	648	1 US-08-185-282-5	

PRED. NO. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### ALIGNMENTS

RESULT 1  
 US-08-657-163A-2

Sequence 2, Application US/08657163A  
 Patent No. 5744449

GENERAL INFORMATION:

APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND THEIR  
 TITLE OF INVENTION: SYNTHETIC LIPPS AND THEIR  
 NUMBER OF SEQUNECES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.  
 CITY: BELLAIR  
 STATE: TEXAS  
 COUNTRY: USA  
 ZIP: 77401

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB  
 COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08-657-163A  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/310,340  
 FILING DATE: 22 SEPTEMBER 1994  
 CLASSIFICATION: 514  
 APPLICATION NUMBER: 08/058,387  
 FILING DATE: 10 MAY 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JOHN R. CASPERSON  
 REGISTRATION NUMBER: 28,198  
 REFERENCE/DOCKET NUMBER: FWL-PAT-US-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713-482-2961  
 TELEFAX: 713-663-7290  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10  
 TYPE: AMINO ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N

ORIGINAL SOURCE: SYNTHETIC  
US-08-657-163A-2

Query Match 100.0%; Score 54; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.004; Mismatches 0; Index 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Index 0; Gaps 0;  
QY 1 LKAMDPTPPI 10  
Db 1 LKAMDPTPPL 10

## RESULT 2

US-08-310-340B-1

Sequence 1: Application US/08310340A  
Patent No. 5576297  
GENERAL INFORMATION:  
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
TITLE OF INVENTION: SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR  
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BINIE V. LIPPS  
STREET: 4509 MIMOSA DR.  
CITY: BELLAIRE  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77401

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB  
COMPUTER: IBM COMPATIBLE  
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/310-340A  
FILING DATE: 22 SEPTEMBER 1994  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/058, 387  
FILING DATE: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME:  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-723-6245  
TELEFAX: 713-663-7290

TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15

HYPOTHETICAL: NO  
TYPE: AMINO ACID  
STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1  
INDIVIDUAL ISOLATE: TEXAS WILD  
DEVELOPMENTAL STAGE: ADULT  
HAPLOTYPE:  
TISSUE TYPE: BLOOD

CELL TYPE:  
CELL LINE:  
ORGANISM:  
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:  
LIBRARY:  
CLONE:

PUBLICATION INFORMATION:  
PUBLICATION INFORMATION:

AUTHORS: JONAS PERALES, ET AL.  
TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE  
JOURNAL: INTERNATIONAL SOCIETY ON  
JOURNAL: TOXICOLOGY  
VOLUME: 10TH WORLD CONGRESS ON ANIMAL  
VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,  
VOLUME: SINGAPORE  
ISSUE: PROGRAMME AND ABSTRACTS  
PAGES: 104  
DATE: 3-8 NOV 1991

## RESULT 3

US-08-657-163A-1

Sequence 1: Application US/08657163A  
Patent No. 574449

GENERAL INFORMATION:  
APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
TITLE OF INVENTION: SYNTHETIC LIPNS AND THEIR  
TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BINIE V. LIPPS  
STREET: 4509 MIMOSA DR.  
CITY: BELLAIRE  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77401

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB  
COMPUTER: IBM COMPATIBLE  
OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/657,163A  
FILING DATE:  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/310,340  
FILING DATE: 22 SEPTEMBER 1994  
CLASSIFICATION: 514  
APPLICATION NUMBER: 08/058,387  
FILING DATE: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:  
NAME: JOHN R. CASPERSON  
REGISTRATION NUMBER: 28,198  
REFERENCE/DOCKET NUMBER: FWL-PAT-US-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-482-5961  
TELEFAX: 713-663-7290

TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15

HYPOTHETICAL: NO  
TYPE: AMINO ACID  
STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1  
INDIVIDUAL ISOLATE: NO  
DEVELOPMENTAL STAGE: NO  
HAPLOTYPE:  
TISSUE TYPE: NO

CELL TYPE:  
CELL LINE:  
ORGANISM:  
IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:  
LIBRARY:  
CLONE:  
ORGANISM: DIDELOPHIS VIRGINIANA

PUBLICATION INFORMATION:  
PUBLICATION INFORMATION:

STRAIN: WILD  
 INDIVIDUAL ISOLATE: TEXAS WILD  
 DEVELOPMENTAL STAGE: ADULT  
 HAPLOTYPE:  
 TISSUE TYPE: BLOOD  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:  
 LIBRARY:  
 CLONE:  
 PUBLICATION INFORMATION:  
 AUTHORS: JONAS PERALES, ET AL.  
 TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAB  
 JOURNAL: INTERNATIONAL SOCIETY ON  
 TOXICOLOGY  
 VOLUME: 10TH WORLD CONGRESS ON ANIMAL  
 PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE  
 ISSUE: PROGRAMME AND ABSTRACTS  
 PAGES: 104  
 DATE: 3-8 NOV 1991  
 US-08-657-163A-1

Query Match 100.0%; Score 54; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPL 10  
 Db 1 LKAMDPTPPL 10

RESULT 4  
 US-09-270-767-43223  
 ; Sequence 43223, Application US/09270767  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 43223  
 ; LENGTH: 253  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; FEATURE:  
 ; OTHER INFORMATION: Xaa means any amino acid  
 ; US-09-270-767-43223

Query Match 100.0%; Score 41; DB 4; Length 253;  
 Best Local Similarity 100.0%; Pred. No. 18; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDPPTPPL 10  
 Db 43 MDPPTPPL 49

RESULT 5  
 US-07-57-224B-42  
 ; Sequence 42, Application US/07857224B  
 ; Patent No. 595884  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Benner, Steven A.  
 ; TITLE OF INVENTION: Predicting Folded Structures of Proteins  
 ; NUMBER OF SEQUENCES: 114  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Steven A. Benner  
 ; STREET: Hadlaubstrasse 151  
 ; CITY: Zurich

RESULT 6  
 US-08-602-999A-444  
 ; Sequence 444, Application US/08602999A  
 ; Patent No. 6184205  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARES, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DBR, Channing J.  
 ; APPLICANT: POWKES, Dana M.  
 ; APPLICANT: RIDER, James E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 467  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Peunie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10016-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/602, 999A  
 FILING DATE: 16-FEB-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MISTOCK, S. Leslie  
 REFERENCE/DOCKET NUMBER: 18,872  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 INFORMATION FOR SEQ ID NO: 444:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-602-999A-444

RESULT 7  
 US-09-500-124-444  
 Sequence 444, Application US/09500124  
 Patent No. 6432820  
 GENERAL INFORMATION:  
 APPLICANT: SPARKS, Andrew B.  
 APPLICANT: KAY, Brian K.  
 APPLICANT: THORN, Judith M.  
 APPLICANT: OULLIUM, Lawrence A.  
 APPLICANT: DER, Channing J.  
 APPLICANT: POWLERS, Dana M.  
 APPLICANT: RIDER, James E.  
 TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME  
 NUMBER OF SEQUENCES: 467  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/500,124  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: A. Anders Brookes  
 REFERENCE/DOCKET NUMBER: 36,373  
 REGISTRATION NUMBER: PB369P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 232:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-071-035-232

Query Match 68.5%; Score 37; DB 4; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 4.2; 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 0;

Qy	2 KAMDPPIPL 10	Db	5 RALPPPPL 13

RESULT 8  
 US-09-071-035-232  
 Sequence 232, Application US/09071035  
 Patent No. 6448043  
 GENERAL INFORMATION:  
 APPLICANT: GLI H. Choi  
 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
 NUMBER OF SEQUENCES: 496  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071, 035  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: A. Anders Brookes  
 REFERENCE/DOCKET NUMBER: 36,373  
 REGISTRATION NUMBER: PB369P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 232:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 210 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-071-035-232

Query Match 68.5%; Score 37; DB 4; Length 210;  
 Best Local Similarity 66.7%; Pred. No. 70; 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 2;

Qy	2 KAMDPPIPL 10	Db	24 KPTDPPI 32

RESULT 9  
 US-09-071-035-230  
 Sequence 230, Application US/09071035  
 Patent No. 6448043

GENERAL INFORMATION:  
 APPLICANT: Gil H. Choi  
 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
 NUMBER OF SEQUENCES: 496  
 CORRESPONDENCE ADDRESS: 496  
 ADDRESSEES: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071, 035  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: A. Andrea Brooke  
 REGISTRATION NUMBER: 36,373  
 REFERENCE/DOCKET NUMBER: PB369P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 TELEX/FAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 230:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 256 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

RESULT 10  
 US-09-071-035-230

Sequence Match  
 Best Local Similarity 68.5%; Score 37; DB 4; Length 256;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	2 KAMDPPTPL 10
Db	50 KPDPTPPI 58

GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 FILE REFERENCE: 012796-032  
 CURRENT APPLICATION NUMBER: US/09/134,000C  
 CURRENT FILING DATE: 1998-08-13  
 PRIOR APPLICATION NUMBER: US 60/105,778  
 PRIOR FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 6812  
 SEQ ID NO: 6583  
 LENGTH: 306

TYPE: PRT

ORGANISM: Enterococcus faecalis  
 US-09-134-000C-6583

RESULT 11  
 US-09-134-000C-6583

Query Match  
 Best Local Similarity 66.7%; Score 37; DB 4; Length 306;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	2 KAMDPPTPL 10
Db	50 KPDPTPPI 58

GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 FILE REFERENCE: 012796-032  
 CURRENT APPLICATION NUMBER: US/09/134,000C  
 CURRENT FILING DATE: 1998-08-13  
 PRIOR APPLICATION NUMBER: US 60/105,778  
 PRIOR FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 6812  
 SEQ ID NO: 6583  
 LENGTH: 306

TYPE: PRT

ORGANISM: Enterococcus faecalis  
 US-09-134-000C-6583

RESULT 12  
 US-09-489-039A-13655

Query Match  
 Best Local Similarity 66.5%; Score 37; DB 4; Length 306;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	2 KAMDPPTPL 10
Db	50 KPDPTPPI 58

GENERAL INFORMATION:  
 APPLICANT: Gary Breton et. al  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 FILE REFERENCE: 2709-2005001  
 CURRENT APPLICATION NUMBER: US/09/489,039A  
 CURRENT FILING DATE: 2000-01-27  
 PRIOR APPLICATION NUMBER: US 60/117,747  
 PRIOR FILING DATE: 1999-01-29  
 NUMBER OF SEQ ID NOS: 14342  
 SEQ ID NO: 13655  
 LENGTH: 323

TYPE: PRT

ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-13655

RESULT 13  
 US-09-248-796A-20624

Query Match  
 Best Local Similarity 66.7%; Score 36; DB 4; Length 323;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1 LKAMDPPTP 9
Db	6 LKAMDALPP 14

GENERAL INFORMATION:  
 APPLICANT: Keith Weinstock et al  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAI  
 FILE REFERENCE: 107196-132

CURRENT APPLICATION NUMBER: US/09/248,790A  
 CURRENT FILING DATE: 1995-02-12

PRIOR APPLICATION NUMBER: US 60/074,725  
 PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 60/096,409 -  
 NUMBER OF SEQ ID NOS: 28208  
 SEQ ID NO 20624  
 LENGTH: 338

TYPE: PRT  
 ORGANISM: Candida albicans

US-09-248-790A-20024

Query Match 66.7%; Score 36; DB 4; Length 338;

Best Local Similarity 77.8%; Pred. No. 1.7e+02; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	2	KAKDPTPPL	10
Db	88	KAKDPTDPL	96

RESULT 14  
 US-09-270-767-57016

; Sequence 57016, Application US/09270767  
 ; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7328-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 57016.

; LENGTH: 27  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster

US-09-270-767-57016

Query Match 64.8%; Score 35; DB 4; Length 27;  
 Best Local Similarity 55.6%; Pred. No. 17; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy	1	LKAKDPTPPL	9
Db	19	LRPLDPSPPP	27

RESULT 15  
 US-09-538-092-166

; Sequence 166, Application US/09538092  
 ; Patent No. 675314

; GENERAL INFORMATION:

; APPLICANT: Giot, Loic

; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09/538,092

; CURRENT FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/178,965

; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 1387  
 ; SOFTWARE: CuraPatSeqFormatter Version 0.9

; SEQ ID NO 166  
 ; LENGTH: 206

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

; NAME/KEY: misc\_feature

; LOCATION: (0)..(0)

; OTHER INFORMATION: Polypeptide Accession Number YDR167W  
 ; US-09-538-092-166

Query Match 64.8%; Score 35; DB 4; Length 206;  
 Best Local Similarity 60.0%; Pred. No. 1.5e+02; Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy	1	LKAKDPTPPL	10
Db	78	LEMMDSTPPI	87

Search completed: January 6, 2005, 10:25:05  
 Job time : 21.2703 Secs



**RESULT 3**  
**E75099** hypothetical protein PAB1590 - *Pyrococcus abyssi* (strain Orsay)  
**C;Species:** Pyrococcus abyssi  
**C;Date:** 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
**C;Accession:** E75099  
**R;anonymous, Genoscope**  
**submitted to the EMBL Data Library, July 1999**  
**A;Reference number:** A75001  
**A;Accession:** E75099  
**A;Status:** preliminary  
**A;Molecule type:** DNA  
**A;Residues:** 1-695 <KAW>  
**A;Cross-references:** UNIPROT:Q9UZG1; GB:AJ248286; GB:AL096836; NID:95458366; PIDN:CA55009  
**A;Experimental source:** strain Orsay  
**C;Genetics:**  
**A;Gene:** PAB1590

**Query Match** 52.4%; Score 44; DB 2; Length 695;  
**Best Local Similarity** 54.5%; **Pred.** No. 36; **Mismatches** 6; **Conservative** 3; **Indels** 0; **Gaps** 0;  
**Matches** 2; **DB** 561 AND PKPPMMILB 571

**RESULT 4**  
**T38769** hypothetical protein SPAC3H8.11 - fission yeast (*Schizosaccharomyces pombe*)  
**C;Species:** Schizosaccharomyces pombe  
**C;Date:** 20-Oct-2000 #sequence\_revision 08-Dec-2000 #text\_change 09-Jul-2004  
**C;Accession:** T38769; T88072  
**R;Gentiles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.**  
**submitted to the EMBL Data Library, January 1996**  
**A;Reference number:** 221810  
**A;Accession:** T38769  
**A;Molecule type:** DNA  
**A;Residues:** 1-105 <GEN>  
**A;Cross-references:** UNIPROT:Q10145; EMBL:260086; NID:91177658; PIDN:CAA93168.1; PID:9117  
**A;Experimental source:** strain 9721-; cosmid c3H8  
**R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.**  
**A;Reference number:** 221810  
**A;Accession:** T38072  
**A;Molecule type:** DNA  
**A;Residues:** 90-777 <CON>  
**A;Cross-references:** EMBL:ZT0690; NID:91256511; PIDN:CA94619.1; PID:93859771; GSPDB:GN00  
**A;Experimental source:** strain 9721-; cosmid c1F3  
**C;Genetics:**  
**A;Gene:** spaci3.01; SPDB:SPAC3H8.11; SPDB:SPAC1F3.01  
**A;Map position:** 1

**Query Match** 52.4%; **Score** 44; **DB** 2; **Length** 777;  
**Best Local Similarity** 46.2%; **Pred.** No. 41; **Mismatches** 6; **Conservative** 4; **Indels** 0; **Gaps** 0;  
**Matches** 3; **DB** 212 SVDETEPIWSTE 224

**RESULT 5**  
**T09402** immunoglobulin-like protein IGSP1 - human  
**C;Species:** Homo sapiens (man)  
**C;Date:** 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
**C;Accession:** T09402  
**R;Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger, D.**

**Genomics** 48, 157-162, 1998  
**A;Title:** Cloning and expression of an immunoglobulin superfamily gene (IGSP1) in *Xq25*.  
**A;Reference number:** Z16655; MUID:98190514; PMID:9521868  
**A;Accession:** T09402  
**A;Status:** preliminary  
**A;Cross-references:** UNIPROT:Q9UZG1; EMBL:AF034198; NID:92645889; PIDN:AC52057.1; PID:92  
**A;Residue:** 1-1327 <MAZ>  
**A;Cross-references:** UNIPROT:O15070; EMBL:AF034198; NID:92645889; PIDN:AC52057.1; PID:92  
**A;Genetics:**  
**A;Gene:** igsp1  
**A;Map position:** Xq25

**Query Match** 52.4%; **Score** 44; **DB** 2; **Length** 1327;  
**Best Local Similarity** 63.6%; **Pred.** No. 75; **Mismatches** 7; **Conservative** 2; **Indels** 0; **Gaps** 0;  
**Matches** 2; **DB** 25 MDPQBELWIES 35

**RESULT 6**  
**AB0644** probable glycosyl hydrolase STY1249 [imported] - *Salmonella enterica* subsp. *enterica* ser. *Typhi*  
**C;Species:** *Salmonella enterica* subsp. *enterica* serovar *Typhi*  
**A;Note:** This species has also been called *Salmonella typhi*  
**C;Accession:** AB0644  
**C;Date:** 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
**C;Accession:** AB0644  
**R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.**  
**Nature** 413, 848-852, 2001  
**A;Authors:** Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
**A;Title:** Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar *Typhi*  
**A;Reference number:** AB0502; MUID:2153497; PMID:11677608  
**A;Accession:** AB0644  
**A;Status:** preliminary  
**A;Molecule type:** DNA  
**A;Cross-references:** GB:AL513382; PIDN:CA00833.1; PID:916502378; GSPDB:GN00176  
**A;Genetics:**  
**A;Gene:** STY1249

**Query Match** 51.2%; **Score** 43; **DB** 2; **Length** 341;  
**Best Local Similarity** 47.1%; **Pred.** No. 24; **Mismatches** 8; **Conservative** 3; **Indels** 2; **Gaps** 4; **DB** 217 RAIDPRPASGPSPWIKT 233

**RESULT 7**  
**D86314** hypothetical protein PAB15.14 - *Arabidopsis thaliana*  
**C;Species:** Arabidopsis thaliana (mouse-ear cress)  
**C;Date:** 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 16-Aug-2004  
**C;Accession:** D86314  
**R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, D.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huijzer, L.**  
**Nature** 408, 816-820, 2000  
**A;Authors:** Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; A.C.; Li, J.H.; Li, Y.; Lin, X.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzali, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
**A;Title:** Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
**A;Reference number:** A86141; MUID:21016719; PMID:1130712  
**A;Accession:** D86314  
**A;Status:** preliminary  
**A;Molecule type:** DNA  
**A;Residues:** 1-687 <STo>

A;Cross-references: UNIPROT:Q9LMT8; GB:AB005172; NID:9665069; PIDN:AAF97271.1; GSPPDB:GN  
 C;Genetics:  
 A;Map position: 1  
 C;Superfamily: homeobox homology  
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 51.2%; Score 43; DB 2; Length 687;  
 Best Local Similarity 46.7%; Pred. No. 52;  
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPLWIKR 15  
 : : ||||| :  
 Db 225 LRLLQTNEPPLWIKRD 239

RESULT 8

A31898 hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - sea urchin (Strongylocentrotus purpuratus (purple urchin))  
 C;Species: Strongylocentrotus purpuratus (purple urchin)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: A31898; A28367  
 R;Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.  
 J. Biol. Chem. 263, 18411-18418, 1988  
 A;Title: 3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin embryo. Deduced  
 A;Reference number: A31898; MUID:89054023; PMID:3192541  
 A;Accession: A31898  
 A;Residues: 1-932 <WOO>  
 A;Molecule type: mRNA  
 A;Note: the authors rearranged portions of the coding region in Figure 2, and the above  
 submitted to Genbank  
 A;Note: the authors translated the codon GCA for residue 805 as Glu  
 R;Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.  
 J. Biol. Chem. 263, 253-257, 1988  
 A;Title: 3-hydroxy-3-methylglutaryl coenzyme A reductase in the sea urchin embryo is dev  
 A;Reference number: A28367; MUID:80115403; PMID:3276692  
 A;Accession: A28367  
 A;Residue: 689-735 <W02>  
 C;Comment: This transmembrane glycoprotein of the endoplasmic reticulum is involved in t  
 C;Superfamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase  
 C;Keywords: cholesterol biosynthesis; coenzyme A; endoplasmic reticulum; glycoprotein; N  
 F;279,850,886,930/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 51.2%; Score 43; DB 1; Length 932;  
 Best Local Similarity 70.0%; Pred. No. 73;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMDPPTPLW 11  
 : ||| ||| |||  
 Db 298 KKIDPPTPLW 307

RESULT 9

D1194 hypothetical protein PH1828 - Pyrococcus horikoshii  
 C;Species: Pyrococcus horikoshii  
 C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
 C;Accession: D1194  
 R;Kawarabayashi, Y.; Savada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir  
 M.; Onifuku, Y.; Funakoshi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
 DNA Res. 5, 55-76, 1998  
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
 A;Reference number: A71000; MUID:98344137; PMID:9679194  
 A;Accession: D1194  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-115 <KAW>  
 A;Cross-references: UNIPROT:O59492; GB:AP000007; NID:93236134; PIDN:BA30947.1; PID:9325  
 A;Experimental source: strain OT3  
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 A;Gene: PH1828

Query Match 50.0%; Score 42; DB 2; Length 115;  
 Best Local Similarity 66.7%; Pred. No. 10; 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDTPPLW 12  
 : : |||||  
 Db 89 ISPSPPPLWI 97

RESULT 10

A87177 conserved hypothetical protein TC0305 [imported] - Chlamydia muridarum (strain Nigg)  
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C;Accession: A87177  
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, V  
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S  
 Nucleic Acids Res. 28, 1397-1406, 2000  
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
 A;Reference number: A81500; MUID:2015025; PMID:10684935  
 A;Accession: A81500  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-398 <TET>  
 A;Cross-references: UNIPROT:O9PL02; GB:AB002298; GB:AB002160; NID:97190343; PIDN:AAF3917  
 A;Experimental source: strain Nigg (MoPn)  
 C;Superfamily: C;Genetics:  
 A;Gene: TC0306  
 C;Superfamily: Chlamydia trachomatis hypothetical protein CT036  
 Query Match 50.0%; Score 42; DB 2; Length 398;  
 Best Local Similarity 77.8%; Pred. No. 41; 1; Mismatches 1; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KAMDPPTPL 10  
 : |||||  
 Db 309 KKIDPPTPL 317

RESULT 11

T04646 aspartate transaminase (EC 2.6.1.1) precursor, chloroplast - Arabidopsis thaliana  
 N;Alternate names: aspartate aminotransferase; protein F10N7\_200  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 09-Jul-2004  
 C;Accession: T04646; S56657; S47490  
 R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohneisel, J.; Mewes, H.W.; Mayer, K.F.X.  
 submitted to the Protein Sequence Database, March 1999  
 A;Reference number: Z15263  
 A;Accession: T04646  
 A;Molecule type: DNA  
 A;Cross-references: UNIPROT:P46248; EMBL:AL021635  
 A;Experimental source: cultivar Columbia; BAC clone F10N7  
 R;Wilkie, S.B.; Roper, J.M.; Smith, A.G.; Warren, M.J.  
 Plant Mol. Biol. 27, 1227-1233, 1995  
 A;Title: Isolation, characterisation and expression of a cDNA clone encoding plastid asp  
 A;Reference number: S56657; MUID:95284373; PMID:776905  
 A;Accession: S56657  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-21, <NV>, 24-453 <WIL>  
 A;Cross-references: EMBL:X81026; NID:9531554; PIDN:CAA56932.1; PID:9531555  
 C;Genetics:  
 A;Gene: aat1  
 A;Map position: 4  
 A;Genome: nuclear  
 A;Intron: 20/3; 37/3; 102/3; 115/3; 145/3; 182/1; 218/3; 265/3; 322/2; 410/3  
 A;Note: F10N7\_200  
 C;Superfamily: aspartate aminotransferase  
 C;Keywords: amino transferase; chloroplast; phosphoprotein; pyridoxal phosphate  
 F;298/Binding site: pyridoxal phosphate (Iys) (covalent) #status predicted

Query Match 50.0%; Score 42; DB 2; Length 453;  
 Best Local Similarity 60.0%; Pred. No. 47; Indels 2; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 2;

Qy :|||:|||:|||:  
 Db 238 IDPTPEQWIK 247

**RESULT 12**

VKXPMV  
 major structural nucleoprotein - Machupo virus  
 N;Alternate names: nucleocapsid protein  
 C;Species: Machupo virus  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C;Accession: S31042  
 R;Griffiths, C.; Wilson, S.M.; Cligg, J.C.S.  
 submitted to the EMBL Data Library, October 1991  
 A;Description: Sequence of the nucleocapsid gene of Machupo virus: close relationship with other arenaviruses  
 A;Reference number: S18042  
 A;Accession: S18042  
 A;Molecule type: genomic RNA  
 A;Residues: 1-1564 <GRI>  
 A;Cross-references: UNIPROT:P26578; EMBL:X62616; NID:960621; PID:CAM4486.1; PID:960622  
 C;Genetics:  
 C;Map position: segment S  
 C;Superfamily: arenavirus major nucleoprotein  
 C;Keywords: nucleocapsid; nucleoprotein

Query Match 50.0%; Score 42; DB 1; Length 564;  
 Best Local Similarity 46.7%; Pred. No. 60; Indels 5; Gaps 0;  
 Matches 7; Conservative 3; Mismatches 5;

Qy :|||:|||:|||:  
 Db 368 VKKLDPTNTWLDIB 382

**RESULT 13**

A29900  
 fasciclin I precursor - American bird grasshopper  
 C;Species: Schistocerca americana (American bird grasshopper)  
 C;Date: 22-Aug-1998 #sequence\_revision 22-Aug-1998 #text\_change 09-Jul-2004  
 C;Accession: A29900; A31817  
 R;Zinn, K.; McAllister, L.; Goodman, C.S.  
 Cell 53, 577-587, 1988  
 A;Title: Sequence analysis and neuronal expression of fasciclin I in grasshopper and Drosophila melanogaster  
 A;Reference number: A29900; MUID:88223351; PMID:3370670  
 A;Accession: A29900  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-662 <ZIN>  
 A;Cross-references: UNIPROT:P10675; GB:M20544; GB:J03787; NID:9160846; PID:gi160847  
 R;Snow, P.M.; Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Bastiani, M.J.;  
 Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988  
 A;Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in t  
 A;Reference number: A94202; MUID:882276943; PMID:2839842  
 A;Accession: A31817  
 A;Molecule type: mRNA  
 A;Residues: 25-42 <SNO>  
 A;Cross-references: EMBL:M20544; EMBL:J03787

Query Match 50.0%; Score 42; DB 2; Length 662;  
 Best Local Similarity 58.3%; Pred. No. 72; Indels 4; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 2;

Qy :|||:|||:|||:  
 Db 104 LSBLDGNPPWIKI 115

RESULT 14

330146  
 ribosomal protein S13, cytosolic - maize  
 C;Species: Zea mays (maize)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: S30146  
 R;Joinin, P.; Gigot, C.; Phillips, G.  
 Plant Mol. Biol. 21, 701-704, 1993  
 A;Title: cDNA nucleotide sequence and expression of a maize cytoplasmic ribosomal protein S13  
 A;Reference number: S30146; MUID:93192530; PMID:8448368  
 A;Accession: S30146  
 A;Molecule type: mRNA  
 A;Residues: 1-151 <JOA>  
 A;Cross-references: UNIPROT:Q05761; EMBL:X2455; NID:9288058; PID:CAM4311.1; PID:9288C  
 C;Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology  
 C;Keywords: protein biosynthesis; ribosome  
 R;2-151/Product: ribosomal protein S13 #status Predicted <MAT>  
 R;82-148/Domain: eubacterial ribosomal protein S15 homology <BS15>  

Query Match 48.8%; Score 41; DB 1; Length 151;  
 Best Local Similarity 75.0%; Pred. No. 20; Indels 6; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 1;

Qy :|||:|||:  
 Db 21 TPPLWKT 28

**RESULT 15**

JC5882  
 myocyte enhancer factor 2B-2 - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 11-Mar-1998 #sequence\_revision 11-Mar-1998 #text\_change 09-Jul-2004  
 C;Accession: JC5882  
 R;Morisaki, T.; Semrauwitayawong, K.; Byun, S.H.; Matsuda, Y.; Hidaka, K.; Morisaki, H.;  
 J. Biochem. 122, 939-946, 1997  
 A;Title: Mouse Mef2B gene: Unique member of MEF2 gene family.  
 A;Reference number: JC5881; MUID:98104045; PMID:9443808  
 A;Accession: JC5882  
 A;Molecule type: DNA  
 A;Residues: 1-339 <MOR>  
 A;Cross-references: UNIPROT:O55097; DDBJ:D87828  
 C;Genetics:  
 C;Comment: This factor plays a differentiation of myocytes, including cardiomyocytes.  
 C;Gene: Mef2b  
 A;Map position: 8  
 F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>  

Query Match 48.8%; Score 41; DB 2; Length 339;  
 Best Local Similarity 61.5%; Pred. No. 50; Indels 8; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 3;

Qy :|||:|||:  
 Db 281 ASPPRPPVSKSE 293

Search completed: January 6, 2005, 10:23:48  
 Job time : 25.5135 secs

GenCore version 5.1.6  
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## On protein - protein search, using SW model

Run on: January 6, 2005, 10:00:35 ; Search time 128.514 seconds  
(without alignments)  
67.157 Million cell updates/sec

Title: US-10-047-945-2  
Perfect score: 84  
Sequence: 1 LKAMDPTPLWIKTE 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqb, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02-\*  
1: uniprot\_sprot:  
2: uniprot\_trembl:  
\* -

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	84	100.0	17	2	Q9TR78
2	84	100.0	291	1	DM43 DIDMR
3	75	89.3	140	2	Q8HZT5
4	75	89.3	291	2	Q8HZT4
5	63	75.0	314	2	Q8HZX5
6	52	61.9	504	2	Q8MS3
7	50	59.5	227	2	Q73ZB2
8	50	59.5	227	2	AAS24008
9	48	57.1	344	2	Q7MTO9
10	47	56.0	51	2	Q8FB0
11	47	56.0	351	1	Y4VU RHISN
12	46	54.8	370	2	Q7QB8
13	46	54.8	634	2	Q9VQP3
14	46	54.8	854	2	Q9VP4
15	46	54.8	856	2	Q9GZ10
16	46	54.8	1017	2	Q7KU30
17	46	54.8	1017	2	AS64617
18	46	54.8	1221	1	TAF2 DROMB
19	45	53.6	97	2	Q91ME9
20	45	53.6	97	2	Q91PB3
21	45	53.6	128	2	Q83V1
22	45	53.6	312	2	Q9N126
23	45	53.6	467	2	Q7YQ07
24	45	53.6	477	2	Q8150
25	44	52.4	125	2	Q9NV61
26	44	52.4	242	2	Q8NB6C5
27	44	52.4	242	2	Q8BX6
28	44	52.4	287	2	Q8HZT2
29	44	52.4	287	2	Q8HZT3
30	44	52.4	377	2	Q9TZ32
31	44	52.4	695	2	Q9UZG1

RESULT 1		PRELIMINARY;		PRT;	17 AA.
ID	Q9TR78	ID	Q9TR78	DT	01-MAY-2000 (TREMBLrel. 13, Created)
AC		DT		DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
QT		DT		DT	01-MAR-2001 (TREMBLrel. 15, Last annotation update)
DB		OS		OS	ANTI-BOTHRIC complex 4000 SUBUNIT (Fragment).
		OS		OS	Didelphis marsupialis (Southern opossum).
		OC		OC	Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi; Mammalia; Metabacteria; Didelphiomorpha; Didelphidae; Didelphis.
		OX		OX	NCBI_TAXID=9268;
		RN		RN	[1]
		RP		RP	SEQUENCE.
		RA		RA	Medline=95149299; PubMed=17466694;
		RT		RT	Parales J., Mousatche H., Marangoni S., Oliveira B., Domont G.B.; Isolation and partial characterization of an anti-bothropic complex from the serum of South American Didelphidae. Toxicon 32:1237-1249(1994);
		RL		RL	SEQUENCE ID: CB55FB0E73B2A CRC64;
		SQ		SQ	17 AA; 1947 MW;

RESULT 2					
Query	Match	Best Local Similarity	Score	Pred. No.	DB 2;
DM43 DIDMR	DM43 DIDMR	STANDARD;	PRT;	291 AA.	
AC	AC				
Q9TR78	P2957;				
	DT	16-OCT-2001 (Rel. 40, Created)			
	DT	28-FEB-2003 (Rel. 41, Last sequence update)			
	DT	05-JUL-2004 (Rel. 44, Last annotation update)			
	DB	Venom metalloproteinase inhibitor DM43.			
	OS	Didelphis marsupialis (Southern opossum).			
	OC	Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi; Mammalia; Metabacteria; Didelphiomorpha; Didelphidae; Didelphis.			
	OX	NCBI_TAXID=9268;			
	RN	[1]			
	RP	SEQUENCE AND MASS SPECTROMETRY.			
	RC	TISSUE-SERUM;			
	RX	Medline=21935368; PubMed=11815628; DOI=10.1074/jbc.M200589200;			
	RA	Neves-Perreira A.G.C., Perreira J., Fox J.W., Shannon J.D., Makino D.L., Garrett R.C., Domont G.B.,			
	RA	structural and functional analyses of DM43, a snake venom metalloproteinase inhibitor from <i>Didelphis marsupialis</i> serum. J. Biol. Chem. 277:1123-1131(2002).			
	CC	-1- FUNCTION: Metalloproteinase inhibitor.			
	CC	-1- SUBUNIT: Homodimer.			
	CC	-1- TISSUE SPECIFICITY: Blood and milk.			

-1 - PTM: N-glycosylated.

CC NOTE-Ref:[1]

-1 - SIMILARITY: Contains 3 immunoglobulin-like V-type domains.

CC DR InterPro; IPR007110; Ig-like.

CC DR InterPro; IPR011015; LEM-like.

CC DR Pfam; PF0047; Ig; 1.

KW PROSITE; PS5035; Ig\_LIKE; 1.

KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;

KW Metalloprotease inhibitor; Repeating Ig-like V-type 1.

FT DOMAIN 22 79 FT DOMAIN 114 171 FT DOMAIN 191 288

FT DISULFID 28 74 FT DISULFID 121 163

FT DISULFID 213 265 FT DISULFID 23 23

FT CARBOHYD 156 156 FT CARBOHYD 160 160

FT CARBOHYD 175 175 FT CARBOHYD 175 AA; 32390 MW; T1496227869A65B CRC64;

SEQUENCE 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match Best Local Similarity 100.0%; Score 84; DB 1; Length 291; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPPPLWIKTE 15 Qy 1 LKAMDPPPLWIKTE 15

Db 1 LKAMDPPPLWIKTE 15 Db 1 LKAMDPPPLWIKTE 15

RESULT 3

ID Q8H275 PRELIMINARY; PRT; 140 AA.

AC Q8H275; Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DT 01-MAR-2004 (TREMBLrel. 26, Last fragmentation update)

DB Alpha 1B glycoprotein D9P51-D (Fragment).

OS Didelphis marsupialis virginiana (North American opossum).

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis; NCBI\_TaxID=9267;

RN [1] SEQUENCE FROM N.A.

RA Martinez M.B.; Pierce J.R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY131000; AAN69111; -.

DR InterPro; IPR011015; Ig\_Like.

FT NON\_TER 1 FT NON\_TER 140 AA; 15297 MW; B19D071A76AA5A7P CRC64;

SQ SEQUENCE 140 AA; 15297 MW; B19D071A76AA5A7P CRC64;

Query Match Best Local Similarity 89.3%; Score 75; DB 2; Length 140; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKAMDPPPLWIKTE 15 Qy 1 LKAMDPPPLWIKTE 15

Db 42 LKAMDPPPLWIKTE 56 Db 24 LKAMDPPPLWIKTE 38

RESULT 4

Q8H274 PRELIMINARY; PRT; 291 AA..

AC Q8H274; Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

Alpha 1B glycoprotein D9P51 (Fragment).

Didelphis marsupialis virginiana (North American opossum).

Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

NCBI\_TaxID=9267;

RN SEQUENCE FROM N.A.

RA Trujillo M.R.O.; Junqueira-de-Azevedo I.L.M.; Neves-Ferreira A.G.C.,

RA Demont G.B.; Ho P.L.; Perales J.;

RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY163806; AAN69811; -.

DR InterPro; IPR00599; Ig\_Like.

DR InterPro; IPR007110; Ig\_Like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SW00409; Ig; 1.

DR PROSITE; PS50835; Ig\_LIKE; 1.

FT SIGNAL 1 23 FT SIGNAL 1 23

FT CHAIN 24 314 FT CHAIN 24 314

SQ SEQUENCE 314 AA; 34604 MW; 69D55F486D5A5 CRC64;

Query Match Best Local Similarity 75.0%; Score 63; DB 2; Length 314; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPPPLWIKTE 15 Qy 1 LKAMDPPPLWIKTE 15

Db 24 LKAMDPPPLWIKTE 38 Db 24 LKAMDPPPLWIKTE 38

RESULT 5

Q8H275 PRELIMINARY; PRT; 314 AA.

AC Q8H275; Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DB Venom metalloproteinase inhibitor DM43b precursor.

OS Didelphis marsupialis (Southern opossum).

OC Mammalia; Metatheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

NCBI\_TaxID=9268;

RN [1] SEQUENCE FROM N.A.

RA TISSUE-Liver;

RA Trujillo M.R.O.; Junqueira-de-Azevedo I.L.M.; Neves-Ferreira A.G.C.,

RA Demont G.B.; Ho P.L.; Perales J.;

RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY163806; AAN69811; -.

DR InterPro; IPR00599; Ig\_Like.

DR InterPro; IPR007110; Ig\_Like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SW00409; Ig; 1.

DR PROSITE; PS50835; Ig\_LIKE; 1.

FT SIGNAL 1 23 FT SIGNAL 1 23

FT CHAIN 24 314 FT CHAIN 24 314

SQ SEQUENCE 314 AA; 34604 MW; 69D55F486D5A5 CRC64;

Query Match Best Local Similarity 80.0%; Score 63; DB 2; Length 314; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPPPLWIKTE 15 Qy 1 LKAMDPPPLWIKTE 15

Db 24 LKAMDPPPLWIKTE 38 Db 24 LKAMDPPPLWIKTE 38

RESULT 6

Q8MIS3 PRELIMINARY; PRT; 504 AA.

AC Q8MIS3; Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DB Venom myotoxin inhibitor DM64 precursor.

OS Didelphis marsupialis (Southern opossum).

NCBI\_TaxID=9267;

RN [1] SEQUENCE FROM N.A.

RA Martinez M.E.; Pierce J.R.;

RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY131001; AAN69121; -.

DR InterPro; IPR00599; Ig\_Like.

DR InterPro; IPR007110; Ig\_Like.

DR InterPro; IPR011015; LEM\_Like.

DR Pfam; PF00047; Ig; 1.

DR SMART; SW00409; Ig; 1.

DR PROSITE; PS5035; Ig\_LIKE; 1.

FT SIGNAL 1 23 FT SIGNAL 1 23

FT CHAIN 24 314 FT CHAIN 24 314

SQ SEQUENCE 314 AA; 34604 MW; 69D55F486D5A5 CRC64;

Query Match Best Local Similarity 80.0%; Score 63; DB 2; Length 314; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPPPLWIKTE 15 Qy 1 LKAMDPPPLWIKTE 15

Db 24 LKAMDPPPLWIKTE 38 Db 24 LKAMDPPPLWIKTE 38

OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	RESULT 8
OC	Mammalia; Metatheria; Didelphimorpha; Didelphidae; Didelphis.	ASD04008 PRELIMINARY; PRTR; 227 AA.
NCBI_TAXID=9268;	SEQUENCE FROM N.A.	
RT	TISSUE=Liver;	
RX	MEDLINE=22361219; PubMed=12473101;	ASD04008; PRELIMINARY; PRTR; 227 AA.
RA	Rocha S.L., Lomonte B.; Neves-Ferreira A.G., Trugilho M.R., Perales J., Junqueira-De-Azevedo Id I., Ho P.L., Domont G.B., Gutierrez J.M., Bur. J. Biochem. 269:6052-6062(2002).	DT 02-MAR-2004 (TREMBLrel. 27, Created)
RN	[2]	DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
RA	Perales J.;	DE Hypothetical protein.
RT	"Functional analysis of DM64, an antimyotoxic protein with immunoglobulin-like structure from <i>Didelphis marsupialis</i> serum.";	GN MAD1691C.
RX	TISSUE=Liver;	OS Mycobacterium paratuberculosis.
RA	Rocha S.L., Neves-Ferreira A.G.C., Trugilho M.R.O., Junqueira-de-Azevedo I.L.M., Ho P.L., Domont G.B., Perales J., DR EMBL; AY078384; AALB2794.1; -.	OC Bacteria; Actinobacteria; Actinomycetales;
RN	[2]	OC Actinomycetinae; Mycobacteriaceae; Mycobacterium.
RP	SEQUENCE FROM N.A.	OX NCBI_TaxID=1770;
RC		RN [1]
FT	INTERPRO; IPR013599; Ig-like.	RP SEQUENCE FROM N.A.
SO	INTERPRO; IPR010105; IgM-like.	RC STRAIN=k10;
RA	INTERPRO; IPR010105; IgE-like.	RA Id L.; Bannantine J., Zhang Q., Amnonin A., Alt D., Kapur V., DR Submitted (SRP-2003) to the EMBL/GenBank/DBJ databases.
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.	KW HYPOTHETICAL PROTEIN.
DR	HSSP; P24071; IUCT.	SQ SEQUENCE 227 AA; 24027 MW; 952EA4962C0BE199 CRC64;
DR	INTERPRO; IPR013599; Ig.	Query Match Best Local Similarity 79.5%; Score 50; DB 2; Length 227; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DR	INTERPRO; IPR010105; Ig-like.	Db 146 LAALDPPLFLW 11
FT	SIGNAL 1 24 Potential.	Db 146 LAALDPPLFLW 156
SO	CHAIN 25 504 AA; 55975 MW; 0446529A6CBA63B9 CRC64.	Query Match Best Local Similarity 72.7%; Score 50; DB 2; Length 227; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
RA	Query Match Best Local Similarity 61.9%; Score 52; DB 2; Length 504; Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	Db 146 LAALDPPLFLW 156
AC	PRELIMINARY; PRT; 227 AA.	Query Match Best Local Similarity 72.7%; Score 50; DB 2; Length 227; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY	1 LKAMDPPLWLKTE 15	Db 146 LAALDPPLFLW 156
Db	24 LLAMETTPRLWIE 38	Query Match Best Local Similarity 72.7%; Score 50; DB 2; Length 227; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
RA	RESULT 7	Db 146 LAALDPPLFLW 156
Q73ZB2	073ZB2; PRELIMINARY; PRT; 227 AA.	RESULT 9
AC	073ZB2; PRELIMINARY; PRT; 227 AA.	QMTQ9
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	ID QMTQ9 PRELIMINARY; PRT; 344 AA.
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	AC QMTQ9; PRELIMINARY; PRT; 344 AA.
DR	Hypothetical protein.	DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DR	OrdeedLocusName=MAD1691C;	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
OS	Mycobacterium paratuberculosis.	DB Rhodanese-like domain protein.
OC	Bacteria; Actinobacteria; Actinomycetales; Actinomycetales; Corynebacterineae; Mycobacterium; Mycobacterium complex (MAC).	GN OrderedLocusName=PGLB87;
OC	Mycoactetrum avium complex (MAC).	OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC	NCBI_TaxID=1770;	OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales; OC Porphyromonadaceae; Porphyromonas.
RN	[1]	OC Porphyromonadaceae; Porphyromonas.
RP	SEQUENCE FROM N.A.	RN [1]
RC	STRAIN=W83;	RP SEQUENCE FROM N.A.
RX	MEDLINE=22829867; PubMed=12949112;	RC STRAIN=W83;
RA	Nelson K.E., Pleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,	RT MEDLINE=22829867; PubMed=12949112;
RA	Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,	RA Raff D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tailor L., Gray J.,
RA	Haff D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tailor L., Gray J.,	RA Granger D.H., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA	Dewhirst F.E., Fraser C.M.,	RA Dewhirst F.E., Fraser C.M.,
RT	"Complete genome sequence of the oral pathogenic bacterium	RT "Complete genome sequence of the oral pathogenic bacterium
RT	Porphyromonas gingivalis strain W83.";	RT Porphyromonas gingivalis strain W83.";
RL	Embl; AB017233; AAC00408.1; -.	RL J. Bacteriol. 185:5591-5601(2003).
DR	SEQUENCE FROM N.A.	DR EMBL; AB017178; AQ066871.1; -.
DR	STRAIN=k10;	DR TIGR; PG1887; -.
RA	Li L.; Bannantine J., Zhang Q., Amnonin A., Alt D., Kapur V.,	DR GO; GO:004792; P:thiosulfate sulfurtransferase activity; IEA.
RL	Submitted (SRP-2003) to the EMBL/GenBank/DBJ databases.	DR GO; GO:0008272; P:bulfate transport; IEA.
DR	EMBL; AB017233; AAC00408.1; -.	DR InterPro; IPR001307; Thiosulfatetrans.
QY	1 LKAMDPPLWLW 156	DR Pfam; PF00581; Rhodanese; 1.
Db	146 LKAMDPPLWLW 156	DR PROSITE; PS00380; RHODANSE_1; 1.
RA	SEQUENCE 227 AA; 24027 MW; 952EA4962C0BE199 CRC64;	DR PROSITE; PS0206; RHODANSE_3; 1.
RA	Best Local Similarity 72.7%; Score 50; DB 2; Length 227; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	DR Complete proteome.
RA	Best Local Similarity 46.7%; Score 49; DB 2; Length 344; Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;	SQ SEQUENCE 344 AA; 38572 MW; F3D938CD668BF304 CRC64;

Db	199	LSACDPNRPWESR	213	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.ibib-sib.ch/announce">http://www.ibib-sib.ch/announce</a> or send an email to license@ibib-sib.ch).
ID	Q8FNBO	PRELIMINARY;	PRT;	51 AA.	CC
AC	Q8FNBO;				CC
DT	01-MAR-2003	(TREMBREL. 23; Last sequence update)	DR		CC
DT	01-MAR-2003	(TREMBREL. 23; Last annotation update)	DR		CC
DR		Hypothetical protein	DR		CC
GN		Orderedcoccusnames-CB235;	DR		CC
OS		Corynebacterium efficiens	DR		CC
OC		Bacteria; Actinobacteridae; Actinomycetales;	DR		CC
OC		Corynebacterineae; Corynebacteriaceae; Corynebacterium.	DR		CC
OX		NCBI_TaxID=152794;	DR		CC
RN		SEQUENCE FROM N.A.	DR		CC
RP		STRAIN=Y5-314;	DR		CC
RX		MEDLINEB-2272752; PubMed=12840036;	DR		CC
RA	Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura B.,		DR		CC
RA	Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,		DR		CC
RA	Gelobori T.;	"Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.", Genome Res. 13:1572-1579(2003).	DR		CC
RT		Complete proteome; Hypothetical protein.	DR		CC
RT		SEQUENCE 51 AA; 5686 MW; 759FC5BDCCB414A CRC64;	DR		CC
RT		Query Match 56.0%; Score 47; DB 2; Length 51; Best Local Similarity 50.0%; Pred. No. 5.6; Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;	DR		CC
Qy	3	AMDPPIPLMKT 14	DR		CC
Qy	21	SLDPPTPRVWET 32	DR		CC
Db		RESULT 11	DR		CC
Y4VJ	RHISN	STANDARD;	PRT;	351 AA.	CC
ID	Y4VJ_RHISN				CC
AC	Q3218;				CC
DT	01-NOV-1997	(Rel. 35, Created)	DR		CC
DT	01-NOV-1997	(Rel. 35, last sequence update)	DR		CC
DT	05-JUL-2004	(Rel. 44, last annotation update)	DR		CC
DB		Hypothetical 39.2 kDa protein Y4VJ.	DR		CC
GN		ORFName=y4vj;	DR		CC
OS		Rhizobium sp. (strain NGR234).	DR		CC
OC		Plasmid sym_PNGR234a.	DR		CC
OC		Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.	DR		CC
OC		NCBI_TaxID=394;	DR		CC
RN	[1]	SEQUENCE FROM N.A.	DR		CC
RP		MEDLINEB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Fellay R., Broughton W.J., Rosenthal A., Perret X.;	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Fellay R., Broughton W.J., Rosenthal A., Perret X.;	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
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RA	Freiberg C.A., Fellay R., Broughton W.J., Rosenthal A., Perret X.;	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
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RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
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RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
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RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
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RT		SEQUENCE FROM N.A.	DR		CC
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RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM N.A.	DR		CC
RP		MEDLINEB-96389014; PubMed=8796346;	DR		CC
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.,	"sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp. NGR234 using dye terminators and a thermostable sequenase: a beginning.", Genome Res. 6:590-600(1996).	DR		CC
RL		-1 SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.	DR		CC
RT		SEQUENCE FROM N.A.	DR		CC
RT		MedlineB-97305956; PubMed=9163424;	DR		CC
RA	Freiberg C.A., Perret X., Broughton W.J., Rosenthal A.,	"Molecular basis of symbiosis between Rhizobium and legumes.", Nature 387:394-401(1997).	DR		CC
RA		SEQUENCE OF 1-279 FROM			

- DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DB CG3327-PB  
 GN Name=EG23; ORFName=CG3327;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriodea; Drosophilidae; Drosophila.  
 OK NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINS=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,  
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler J.H., Cadieu B., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
 RA de Pablo B., Deicher A., Deng Z., Mayr A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Douc L.E., Downey M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin R.J., Evangelista C.C., Ferrall S., Ferreira S., Fleischmann W.,  
 RA Rosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glaser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan J., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernández J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibsegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei M., McIntosh B., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mibarry C., Morris J., Mosbrfsl A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson N.A., Nixon K., Nuskeen D.R., Paclek J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler P., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simonsen M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhou X., Zhu S.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;  
 RA Patel S., Adams M., Champé M., Dugan S.P., Frise E., Hodson A.,  
 RA George R.A., Hoskins R.A., Laverty T., Muñoz D.M., Nelson C.R.,  
 RA Peclb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirkas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
 RT melanogaster euchromatic genome sequence.",  
 RT Genome Biol. 3:RESEARCH0079(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINS=2242605; PubMed=12537573;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,  
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINS=2242609; PubMed=12537572;  
 RA Misra S., Crosby M.A., Munigall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Roabro S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Galbart W.M., Rubin G.M.,  
 RA Lewis S.B.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 systematic review.", Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINS=2242610; PubMed=12537571;  
 RA FLYBASE;  
 RA Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  
 CC -1-SIMILARITY: Belongs to the ABC transporter family.  
 EMBL: AB00380; AF51122.2; -.  
 DR FLYBase: FBgn0020445; B23.  
 DR GO; GO:0016202; C:membrane; IEA.  
 DR GO; GO:000524; P:ATP binding; IEA.  
 DR GO; GO:0004009; P:ATP-binding cassette (ABC) transporter acti... ; IEA.  
 DR GO; GO:0001661; P:nucleotide binding; IEA.  
 DR GO; GO:0068101; P:transport; IEA.  
 DR InterPro: IPR00593; AAA ATPase.  
 DR InterPro: IPR03439; ABC Transporter.  
 DR Pf00005; ABC tran; 1.  
 DR SMART: SM00382; AAA; 1.  
 DR PROSITE: PS00211; ABC TRANSPORTER\_1; 1.  
 DR PROSITE: PS0893; ABC TRANSPORTER\_2; 1.  
 KW ATP-binding.  
 SO SEQUENCE ID: 634 AA; 7223 MW; ARD0300DCDB04B01 CRC64;  
 ID Q9VQPA  
 AC Q9VQPA4  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DB CG3327-PA.  
 GN Name=EG23; ORFName=CG3327;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriodea; Drosophilidae; Drosophila.  
 OK NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINS=2019605; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,  
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Genome Biol. 3:RESEARCH0079(2002).  
 RN [3]

RA	Burtis K.D., Cawley S., Dahike B., Davenport L.B., Davries P.,	DR	PROTEIN; FBgn0020445; E23.
RA	Cherry J.M., Cawley S., Dahike B., Davenport L.B., Davries P.,	DR	GO; GO:0016020; C membrane; IFA.
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	DR	GO; GO:000554; F-ATP binding; IFA.
RA	Dobson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	DR	GO; GO:000409; F-nucleotide binding cassette (ABC) transporter acti... ; IFA.
RA	Durban K.J., Evangelista C.C., Ferrera S., Ferreira C., Fleischmann W.,	DR	Harris Pro; IPR003419; ABC transporter.
RA	Fosler C., Gabrieleian A.B., Garg N.S., Gilbert W.M., Glasser K.,	DR	InterPro; IPR003533; ABC transporter.
RA	Gjodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	DR	InterPro; IPR003419; ABC transporter.
RA	Hastin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	DR	Pfam; PF0005; ABC tran...1.
RA	Houston K.A., Howland T.J., Wei M.H., Ikegami C.,	DR	Protein; PDD00006; ABC transporter; 1.
RA	Jalali M., Kalush P., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,	DR	SMART; SM0382; AAA; 1.
RA	Klumper B.B., Kraft C., Kravitz S., Kulp D., Lai Z.,	DR	PROSITE; PS0021; ABC TRANSPORTER_1; 1.
RA	Lasko P., Lei Y., Levitsky A.A., Li J.-J., Li Z., Liang Y., Lin X.,	DR	PROSITE; PS50893; ABC TRANSPORTER_2; 1.
RA	Liu X., Mattes B., McIntosh T.C., McLeod M.P., McPherson D.,	KW	ATP-binding; IFA.
RA	Merkulov G., Milashina N.V., Mobarry C., Morris J.R., Moherfi A.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muony D.M., Nelson D.L.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Paisleb J.M.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Schu B.C., Siden-Kiamos I., Simpson M., Skubski M.P., Smith T.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun B.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Williams S.M., Wodagert M., Worley K., Wu D., Yang S., Yao Q.A., Ye J.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Zheng X.N., Zhou X., Zhou S., Zhu X., Smith H.O.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Gibbs R.A., Myers B.W., Rubin G.M., Venter J. C.;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RT	"The genome sequence of <i>Drosophila melanogaster</i> .";	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RL	Science 287:2185-2195(2000).	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RN	[2]	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RP	SEQUENCE FROM N.A.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RX	MEDLINE-22426065; PubMed=12537568;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Patel S., Adams M., Champé P., Dugan S.P., Frise B., Hodgson A.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	George R.A., Roskin A., Laverty T., Muzy D.M., Nelson C.R.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Pacleb J.M., Bark P., Preiffer B.P., Richards S., Sodergren E.J.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Weinstein G., Scheier S.E., Myers B.W., Gibbs R.A., Rubin G.M.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	"Finishing a whole-genome shotgun: release 3 of the <i>Drosophila melanogaster</i> euchromatic genome sequence.>";	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RT	"The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomic perspective.";	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RT	Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RL	[3]	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RN	SEQUENCE FROM N.A.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RX	MEDLINE-22426070; PubMed=12537573;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	"The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomic perspective.";	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RN	[4]	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RP	SEQUENCE FROM N.A.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RX	MEDLINE-22426079; PubMed=12537579;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Hadley P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Smith C.D., Tupy J.L., Whited B.J., Bayraktaroglu L., Berman B.P.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Bettencourt B.R., Celniker S.B., de Grey A.D., Dysdale R.A.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Stapleton M.L., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Lewis S.E.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RT	"Annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a systematic review.";	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RL	Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RN	[5]	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RP	SEQUENCE FROM N.A.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RG	FLYBASE;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RL	Submitted (MAR-2004) to the EMBL/GenBank/DDJB databases.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
CC	- - - SIMILARITY: Belongs to the ABC transporter family.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	EMBL; AE03550; AAF5121.2; -.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	INTACT; Q9VQ44; -.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	DR	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RP	SEQUENCE FROM N.A.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RG	FLYBASE;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RL	Submitted (SEP-2002) to the EMBL/GenBank/DDJB databases.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RN	[6]	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
QP	Query Match	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DB	Best Local Similarity	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
Matches	57.1%; Pred. No. 1.6e+02; Mismatches 4; Indels 0; Gaps 0;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
QP	1 LKAMDPPTPIWIKT 14	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DB	816 LKAQNTPSPWLN 829	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
Query Match	54.8%; Score 46; DB 2; Length 856;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
Best Local Similarity	57.1%; Pred. No. 1.6e+02; Mismatches 4; Indels 0; Gaps 0;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
Matches	8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
QY	1 LKAMDPPTPIWIKT 14	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DB	814 LKAQNTPSPWLN 827	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RESULT 15		DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
Q9GZ10		DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
ID	Q9GZ10	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
AC	Q9GZ10;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DT	01-MAR-2001 (TREMBL)	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DT	01-MAR-2004 (TREMBL)	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DE	DT	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
GN	E23;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
OS	Bacillus melanogaster (Fruit fly).	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
OC	Ephydriidae; Drosophilidae; Drosophila;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
OX	NCBI_TaxID7227;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RN	[1]	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RP	SEQUENCE FROM N.A.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RX	MEDLINE-20402567; PubMed=10931948;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RA	Hock T., Cotrill T., Keegan J., Garza D.,	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RT	"The E23 early gene of <i>Drosophila</i> encodes an ecdysone-inducible ATP-binding cassette transporter capable of repressing ecdysone-mediated gene activation.";	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
RT	Proc. Natl. Acad. Sci. U.S.A. 97:9519-9524(2000).	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
CC	--! SIMILARITY: Belongs to the ABC transporter family.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	EMBL; AB270799; AAC02041.1; -.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	Flybase; FBgn0020445; E23.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
GO	GO; GO:0016020; C membrane; IFA.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	GO; GO:000554; F-ATP binding; IFA.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	GO; GO:000409; F-ATP-binding cassette (ABC) transporter acti... ; IFA.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	GO; GO:000166; F-nucleotide binding; IFA.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	GO; GO:000680; P-trinitrophenyl ester binding; IFA.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	InterPro; IPR003533; AA-ATPase.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	InterPro; IPR003439; ABC transporter.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
PFAM	PF0005; ABC tran...1.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	SMART; SM0382; AAA; 1.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	PROSITE; PS0021; ABC TRANSPORTER_1; 1.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DR	PROSITE; FS0031; ABC TRANSPORTER_2; 1.	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
KW	ATP-binding	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
SQ	SEQUENCE 856 AA;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
Query Match	54.8%; Score 46; DB 2; Length 856;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
Best Local Similarity	57.1%; Pred. No. 1.6e+02; Mismatches 4; Indels 0; Gaps 0;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
Matches	8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
QY	1 LKAMDPPTPIWIKT 14	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.
DB	816 LKAQNTPSPWLN 829	DR	PROTEIN; FS50893; ABC TRANSPORTER_2; 1.

Thu Jan 6 10:59:27 2005

Search completed: January 6, 2005, 10:17:46  
Job time : 131.514 secs

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## OM protein - protein search, using SW model

Run on: January 6, 2005, 10:08:37 ; Search time 119.189 Seconds  
(without alignments)  
45.146 Million cell updates/sec

Title: US-10-047-945-2  
Perfect score: 84  
Sequence: 1 LKAMDPPTPLWIKTR 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04::\*  
1: geneseqdp1980s::\*  
2: geneseqdp1990s::\*  
3: geneseqdp2000s::\*  
4: geneseqdp2001s::\*  
5: geneseqdp2002s::\*  
6: geneseqdp2003as::\*  
7: geneseqdp2003bs::\*  
8: geneseqdp2004s::\*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1			
ID	Description	PR	PN
AAW11575	AAW11575 standard; peptide; 15 AA.	XX	XX
AAW11575;		AC	
		XX	
		DT	25-MAR-1997 (revised)
		XX	20-MAR-1997 (first entry)
		DE	N-terminal peptide from lethal toxin neutralising factor.
		XX	KW Lethal toxin neutralising factor; LTNF; opossum; bee toxin; scorpion toxin; plant toxin; bacterial toxin; venom; sting; snake bite.
		XX	KW Didelphis virginiana.
		OS	Didelphis virginiana.
		XX	PD 19-NOV-1996.
		XX	PP U5576297-A.
		XX	PR 22-SEP-1994; 94US-00310340.
		XX	PR 10-MAY-1993; 93US-00058387.
		XX	PA (LIPP/) LIPPS B V.
		PA (LIPP/) LIPPS F W.	
		XX	PT LIPPS FW, LIPPS BV;
		XX	DR WPI; 1997-011287/01.
		XX	PT Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal peptide.
		XX	PT Treatment of victims of bee or scorpion stings or plant or bacterial toxins - by admin. of lethal toxin-neutralising factor or its N-terminal peptide.
		PS	Claim 7; Col 9; 9pp; English.
		CC	The present sequence is from the N-terminus of a 68 kD protein purified from the serum of the opossum <i>Didelphis virginiana</i> . The full-length protein is a Lethal toxin neutralising factor (LTNF). The use of purified LTNF or of the chemically synthesised 15mer N-terminal Peptide for treating victims of bee stings, scorpion stings and bacterial or plant toxins is claimed. The patent disclosure does not provide any evidence for neutralising activity against these various toxins. There is evidence of significant neutralising activity of the opossum LTNF and the 15mer peptide against venom from snakes of the families Crotalidae, Elapidae, Hydrophiidae and Viperidae. (Updated on 25-MAR-2003 to correct PP field.)
		CC	AAG54515 Zea mays
		CC	AAG54605 Zea mays
		CC	AAG54604 Zea mays
		CC	AAG54603 Zea mays
		CC	AAB10737 Human pol
		CC	AAB93318 Human pro
		CC	AAB22890 Novel hum
		CC	AAB9051 Human pit
		CC	AAB90617 Human pit
		CC	ABG47496 Breast ca
		CC	ABP1873 Human pro
		CC	AAB32796 Novel hum
		CC	Abh80228 Synthetic
		CC	Abh23550 Protein e
		CC	Abg23871 Novel hum
		CC	Abu47234 Protein e
		CC	Abu45098 Protein e
		CC	Abu47970 Protein e
		CC	Aam79784 Human pro
		CC	AAG27883 Arabidops
		CC	AAG27882 Arabidops
		CC	AAG27881 Arabidops

SQ Sequence 15 AA:  
 Query Match 100.0%; Score 84; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2e-06; 0; Mismatches  
 Matches 15; Conservative 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPWKTE 15  
 Db 1 LKAMDPTPPWKTE 15

RESULT 3  
 ABB80223 Standard; peptide; 15 AA.  
 ID ABB80223  
 XX  
 AC ABB80223;  
 XX  
 DT 06-Nov-2003 (first entry)  
 XX  
 DB Synthetic LTNF, LT-15.  
 XX  
 KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;  
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;  
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;  
 KW SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome;  
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;  
 KW saliva; ELISA.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003060471-A2.  
 XX  
 PD 24-JUL-2003.  
 XX  
 PR 14-JAN-2003; 2003WO-US001044.  
 XX  
 PR 14-JAN-2002; 2002US-00047945.  
 XX  
 PA (LIPPF/) LIPPS B V.  
 PA (LIPPF/) LIPPS F W.  
 XX  
 PI LIPPS BV, LIPPB FW;  
 XX  
 DR WPI; 2003-636703/60.

XX  
 PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.  
 XX  
 PS Claim 3; Page 3; 24pp; English.  
 XX  
 CC The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgG levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythema nodosum (SUB), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA.

XX  
 Sequence 15 AA;  
 Query Match 100.0%; Score 84; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2e-06; 0; Mismatches  
 Matches 15; Conservative 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPWKTE 15  
 Db 1 LKAMDPTPPWKTE 15

RESULT 4  
 ABB80225

RESULT 2  
 AW53841  
 ID AW53841 Standard; peptide; 15 AA.  
 XX  
 AC AW53841;  
 XX  
 DT 08-JUL-1998 (first entry)  
 XX  
 DB N-terminus of opossum LTNF.  
 XX  
 KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy; anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite; sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin; histamine reaction treatment.

XX  
 OS Didelphis virginiana.  
 XX  
 PN US5744449-A.  
 XX  
 PD 28-APR-1998.  
 XX  
 PP 03-JUN-1996; 96US-00657163.  
 XX  
 PR 10-MAY-1993; 93US-00059387.  
 XX  
 PR 22-SEP-1994; 94US-00310340.  
 XX  
 PA (LIPPF/) LIPPS B V.  
 PA (LIPPF/) LIPPS F W.  
 XX  
 PI LIPPS FW, LIPPS BV;  
 XX  
 DR WPI; 1998-271108/24.  
 XX  
 PT This sequence represents the peptide of the invention. It is a lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity to horse proteins.

XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 2; length 15;  
 Best Local Similarity 100.0%; Pred. No. 2e-06; 0; Mismatches  
 Matches 15; Conservative 0; Indels 0; Gaps 0;

QY 1 LKAMDPTPPWKTE 15  
 Db 1 LKAMDPTPPWKTE 15



DB N-terminus of opossum LTNF.  
 XX  
 KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;  
 KW anti-haemorrhagic protein; Elapidae; Viperidae; sea snake; snake bite;  
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;  
 KW histamine reaction treatment.  
 XX OS Didelphis virginiana.  
 XX PN US5744499-A.  
 XX PD 28-APR-1998.  
 XX PR 03-JUN-1996; 96US-00657163.  
 XX PR 10-MAY-1993; 93US-00058387.  
 XX PR 22-SEP-1994; 94US-00310340.  
 XX PA (LIPP/) LIPPS B V.  
 XX PA (LIPP/) LIPPS F W.  
 XX PI LIPPS FW, LIPPS BV;  
 XX DR WPI; 1998-271108/24.  
 XX PT Lethal Toxin Neutralising Factor peptide from opossum - can neutralise  
 venom(s) from all major families of poisonous snakes.  
 XX PS Claim 7; Col 11; lipp; English.  
 XX CC This sequence represents the peptide of the invention. It is a lethal  
 CC toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic  
 protein derived from an opossum. The peptide can be used in a method for  
 CC treating a victim of envenomation from a poisonous snake, preferably a  
 CC poisonous snake from the family of Elapidae, Viperidae or sea snake. It  
 CC is useful for the treatment of snake bites, sepsis, allergies caused by  
 CC the environment and treatment of bee or scorpion stings or toxicities  
 CC caused by plant or bacterial toxins. The peptide can also be used in  
 CC histamine reaction treatment. The peptide can be used in envenomation  
 CC treatment for a variety of snakes without prior identification of the  
 CC snake. Being short it can be synthetically prepared rather than the  
 CC current production in horses, where some people can show hypersensitivity  
 CC to horse proteins  
 XX SQ Sequence 10 AA;

Query	Match	64.3%	Score	54	DB	2	Length	10
Best	Local Similarity	100.0%	Pred.	No.	0.074			
Matches	10	;	Conservative	0				
Oy	1		Mismatches	0				
Dy	1		Indels	0				
			Gaps	0				

RESULT 7  
 ABB80222  
 ID ABB80222 standard; peptide; 10 AA.  
 AC ABB80222;  
 XX DT 06-NOV-2003 (first entry)  
 XX DB Synthetic LTNF, LT-10.  
 XX KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;  
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;  
 KW IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;  
 KW ADA; asthma; diabetes; autoimmune disease; Sjogren's syndrome; Reiter's syndrome;  
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;  
 KW saliva; ELISA.  
 XX OS Synthetic.

XX SQ Sequence 10 AA;

Query	Match	64.3%	Score	54	DB	7	Length	10
Best	Local Similarity	100.0%	Pred.	No.	0.074			
Matches	10	;	Conservative	0				
Oy	1		Mismatches	0				
Dy	1		Indels	0				
			Gaps	0				

RESULT 8  
 ABB80227  
 ID ABB80227 standard; peptide; 9 AA.  
 AC ABB80227;  
 XX DT 06-NOV-2003 (first entry)  
 XX DB Synthetic LTNF, LT-9.  
 XX KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E;  
 KW IgE; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;  
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus;  
 KW IgB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase;  
 KW ADA; asthma; diabetes; autoimmune disease; Sjogren's syndrome; Reiter's syndrome;  
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression;  
 KW saliva; ELISA.  
 XX OS Synthetic.

XX PN WO2003060471-A2.  
 XX PD 24-JUL-2003.  
 XX PR 14-JAN-2003; 2003WO-US001044.  
 XX PR 14-JAN-2002; 2002US-00047945.  
 XX PA (LIPP/) LIPPS B V.  
 XX PA (LIPP/) LIPPS F W.  
 XX PI LIPPS BV, LIPPS FW;  
 XX DR WPI; 2003-636703/60.  
 XX PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, e.g.  
 PT insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g.  
 PT asthma or diabetes, by employing an ELISA on a saliva sample from a  
 PT patient.  
 XX PS Claim 7; Page 3; 24pp; English.  
 XX CC The sequences given in ABB80222-28 represent lethal toxin neutralising  
 CC factor (LTNF). Peptides which may be used for reducing elevated levels of  
 CC serum protein selected by immunoglobulin E (IgE), nerve growth factor  
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In  
 CC particular, the methods of the invention are useful for diagnosing and  
 CC treating conditions with elevated serum IgE levels, e.g. asthma,  
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid  
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,  
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of  
 CC the protein may be monitored by assaying a human endogenous protein by  
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva  
 CC sample using an anti-serum that is specific for the protein. Saliva  
 CC collection is relatively non-invasive when compared to blood collection  
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires  
 CC clotting time before centrifugation to separate serum. Saliva proteins  
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from  
 CC serum requires a more complicated sandwich type ELISA.

XX SQ Sequence 10 AA;

Query	Match	64.3%	Score	54	DB	7	Length	10
Best	Local Similarity	100.0%	Pred.	No.	0.074			
Matches	10	;	Conservative	0				
Oy	1		Mismatches	0				
Dy	1		Indels	0				
			Gaps	0				

RESULT 9  
 ABB80227  
 ID ABB80227 standard; peptide; 9 AA.  
 AC ABB80227;  
 XX DT 06-NOV-2003 (first entry)  
 XX DB Synthetic LTNF, LT-9.

PD 24-JUL-2003.  
 XX PA (HYSE-) HYSEQ INC.  
 PP XX Drmanac RT, Liu C, Tang YT;  
 XX PI  
 PR XX DR -PSDB; AAS82331.  
 XX PA (LIPPP/) LIPPS B V.  
 XX PT (LIPPP/) LIPPS F W.  
 XX PI LIPPS BV, LIPPS FW;  
 XX DR WPI; 2003-636703/60.  
 XX PS Claim 7; Page 4; 24pp; English.  
 XX PT assaying a human endogenous protein (e.g. IgB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.  
 XX PS  
 XX CC The sequences given in ABG0222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin B (IgB), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgB levels e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-*serum* that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA.  
 XX SQ Sequence 9 AA;  
 Query Match 59.5%; Score 50; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LKAMDPTPP 9  
 Db 1 LKAMDPTPP 9  
 RESULT 9  
 ABG18144  
 ID ABG18144 standard; protein; 303 AA.  
 XX AC  
 XX ABG18144;  
 XX DT 18-FEB-2002 (first entry)  
 XX DE Novel human diagnostic protein #18135.  
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; Homo sapiens.  
 XX PN WO200175067-A2.  
 XX PD 11-OCT-2001.  
 XX PR 30-MAR-2001; 2001WO-US008631.  
 XX PR 31-MAR-2000; 2000US-00540217.  
 XX PR 23-AUG-2000; 2000US-00649167.  
 XX OS Homo sapiens.

PA (HYSE-) HYSEQ INC.  
 XX Drmanac RT, Liu C, Tang YT;  
 XX PI  
 PR XX DR -PSDB; AAS82331.  
 XX PA New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.  
 XX PT  
 XX PS Claim 20; SEQ ID NO 48503; 103pp; English.  
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG10377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 303 AA;  
 Query Match 56.0%; Score 47; DB 4; Length 303;  
 Best Local Similarity 42.9%; Pred. No. 34; Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 Oy 2 KAMDPPTPLWIKME 15  
 Db 39 BASDPVPPYWRLQ 52  
 RESULT 10  
 ABR54218  
 ID ABR54218 standard; protein; 531 AA.  
 XX AC ABR54218;  
 XX DT 23-JUN-2003 (first entry)  
 XX DB Human Nov21a protein SEQ ID NO:104.  
 XX KW Human; NOX; antiatherosclerotic; hypotensive; cardiotonic; dermatological; anorectic; immunosuppressive; cytotoxic; antidiabetic; antifertility; haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic; antihypertensive; gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma; congenital heart defect; aortic stenosis; valve disease; transplantation; tuberosclerosis; obesity; congenital adrenal hyperplasia; diabetes; prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer; fertility; haemophilia; hypercoagulation; graft versus host disease; idiopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia; Crohn's disease; multiple sclerosis; infectious disease; cancer; cancer-associated cachexia; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X.

XX	CC	Sequences, which are used in examples from the present invention.	
PN	CC	ABR4277 represents a human trypsinogen protein given in comparison with	
XX	CC	the human NOV35b protein in the exemplification of the present invention	
PD	XX		
XX	SQ	Sequence 531 AA;	
PR	QY	:           15	
09-SEP-2002;	PR	MDPTPPLWIKME 15	
2002WQ-US028538.	Db	70 MDTSPLWLTIE 81	
XX	RESULT 11		
PR	ID	AAY74721	
25-SEP-2001;	PR	AAY74721 standard; protein; 267 AA.	
2001US-0323636P.	XX		
PR	ID	AAY74721	
17-SEP-2001;	PR	AAY74721;	
2001US-032817P.	XX		
PR	ID	AAY74721;	
19-SEP-2001;	PR	21-MAR-2000 (first entry)	
2001US-0323519P.	DT		
PR	ID	Neisseria meningitidis ORF 241 protein sequence SEQ ID No:916.	
17-MAY-2002;	PR	XX	
2002US-0382483P.	KW	Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;	
29-MAY-2002;	PR	KW	antigenic; immunogenic; infection; meningitis; septicemia;
PR	KW	antibacterial; gene therapy.	
05-MAR-2002;	PR	XX	
2002US-0361663P.	OS	Neisseria meningitidis.	
03-MAY-2002;	PR	XX	
2002US-0396412P.	OS	Neisseria meningitidis.	
13-AUG-2002;	PR	XX	
2002US-0403517P.	PN	W0957280-A2.	
06-SEP-2002;	PR	XX	
2002US-00236417.	PD	11-NOV-1999.	
XX	XX		
PA	PP	30-APR-1999;	
(CURA-) CURAGEN CORP.	PP	99W0-US009346.	
XX	XX		
PI	PR	01-MAY-1998;	
Agee ML, Alsobrook JP, Anderson DW, Berghe C, Boldog PU;	PR	98US-0093758P.	
Burgess CE, Casman SJ, Catterton B, Chant JS, Chaudhuri A;	PR	98US-0094699P.	
PI	PB	31-JUL-1998;	
Crabtree J, Dipiro VA, Edinger SR, Eissen AJ, Elerman K;	PB	98US-0098994P.	
PI	PR	02-SEP-1998;	
Gangollie EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusov VV, Ji W;	PR	98US-009962P.	
PI	PR	02-SEP-1998;	
Geekuda R, Khramtsov DV, Leach MD, Lepley DM, Li L, Lin X;	PR	98US-0103749P.	
PI	PR	09-OCT-1998;	
Malyanfar UM, Miller CB, Ort T, Padigaru M, Paturajan M;	PR	98US-0103794P.	
PI	PR	09-OCT-1998;	
Pena CBA, Rieger DK, Rothenberg ME, Shenvoy SG, Shimkets RA;	PR	98US-0103796P.	
PI	PR	09-OCT-1998;	
Spaderna SK, Spyrek KA, Tauzier RJ, Twomlow N, Vernet GM;	PR	98US-0103798P.	
PI	PR	09-OCT-1998;	
Zerhusen BD, Zhong M;	PR	99US-0121528P.	
XX	XX		
XX	PA	(CHIR ) CHIRON CORP.	
PT	PA	(GENO-) INST GENOMIC RES.	
PT	XX		
PS	PR	Frazer C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;	
XX	PI	Peterson J, Pizza M, Rappoli R, Ratti G, Scalato E, Scarbelli M;	
CC	PI	Tettelin H, Venter JC;	
CC	DR	N-PGDB; AAZ53483.	
1 to 42.	DR	WPI; 2000-06215/05.	
ACC62236 to ACC62345 encode the human NOV proteins given in	XX		
ABR54167 to ABR54256.	XX		
NOV sequences have antiatherosclerotic, cardiant,	XX		
hypotensive, dermato logical, anorectic, immunopressive, cytostatic,	XX		
antidiabetic, antiinflammatory, haemostatic, antiinflammatory, anti-HIV,	XX		
antiasthmatic, metabolic, immunomodulator, neuroprotective, nootropic,	XX		
anticarboxin and antilipemic activities, and can be used in gene	XX		
therapy. NOV proteins are useful for treating or preventing a pathology	XX		
associated with a NOV protein in humans and for treating a syndrome	XX		
associated with the human disease. NOV nucleic acids, proteins and	XX		
antibodies can be used in the treatment and diagnosis of cardiomyopathy,	XX		
atherosclerosis, hypertension, congenital heart defects, aortic stenosis,	XX		
valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,	XX		
congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic	XX		
disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,	XX		
hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host	XX		
disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis,	XX		
infectious disease, anoxia, cancer-associated cachexia, cancer,	XX		
Alzheimer's disease, Parkinson's disease, immune disorders,	XX		
hematopoietic disorders, dyslipidaemias, and metabolic syndrome X.	XX		
ACC62346 to ACC62465 represent PCR primers and probes for human NOV.	CC		

CC used in gene therapy protocols  
 XX SQ Sequence 267 AA;  
 SQ Query Match 54.8%; Score 46; DB 3; Length 267;  
 Best Local Similarity 58.3%; Pred. No. 43; 3; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 3;  
 Qy 3 AMDPTPPWIKT 14  
 Db 9 AKHPTPPWIKT 20  
 RESULT 12  
 AAY74718  
 ID AAY74718 standard; protein; 267 AA.  
 XX AC AAY74718;  
 XX DT 21-MAR-2000 (first entry)  
 DB Neisseria meningitidis ORF 241 protein sequence SEQ ID NO:910.  
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;  
 KW antibacterial; gene therapy.  
 OS Neisseria meningitidis.  
 XX PN WO9957280-A2.  
 XX PD 11-NOV-1999.  
 XX PP 30-APR-1999; 99WO-US009346.  
 XX PR 01-MAY-1998; 98US-0083758P.  
 PR 31-JUL-1998; 98US-0094863P.  
 PR 02-SEP-1998; 98US-0098994P.  
 PR 09-OCT-1998; 98US-0103743P.  
 PR 05-OCT-1998; 98US-0103794P.  
 PR 09-OCT-1998; 98US-0103796P.  
 PR 25-FEB-1999; 99US-0121528P.  
 XX PA (CHIR ) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RBS.  
 XX PT Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;  
 PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarbelli M;  
 PI Lettein H, Venter JC;  
 DR WI; 2000-062150/05.  
 DR N-PSDB; A253480.  
 PT Novel Neisserial polypeptides predicted to be useful antigens for  
 vaccines and diagnostics.  
 PS Claim 2; Page 55; 143pp; English.  
 XX CC A253015 to A25536, A25577 to A25615, and AAY75941  
 represent novel Neisseria meningitidis and N. gonorrhoeae polymeric nucleotides  
 and polypeptides. A25457 to A254576 and A254616 to A25573 represent  
 PCR primers used in the amplification of the present invention. The  
 polypeptides, the polynucleotides, antibodies and compositions of the  
 invention can be used as vaccines, as diagnostic reagents, and as  
 immunogenic compositions. The polypeptides can be used in the manufacture  
 of medicaments for treating or preventing infection due to Neisserial  
 bacteria (e.g. meningitis and septicemia), to detect the presence of  
 Neisseria bacteria, or to raise antibodies. They may also be used to  
 screen for agonists or antagonists, which may themselves have use as  
 antibacterial agents. The polynucleotides of the invention may also be  
 used in gene therapy protocols  
 XX SQ Sequence 729 AA;  
 SQ Query Match 54.8%; Score 46; DB 4; Length 729;  
 Best Local Similarity 57.1%; Pred. No. 1.2e+02; 4; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 4;  
 Qy 1 IAKMDPTPPWIKT 14  
 Db 689 LKAQNSTSPMLKT 702  
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 XX AC ABB59797;  
 XX DT 26-MAR-2002 (first entry)  
 DB Drosophila melanogaster polypeptide SEQ ID NO 6183.  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PR 23-MAR-2001; 2001WO-US009331.  
 XX PR 23-MAR-2000; 2000US-019167P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX PR (PBKR ) PB CORP NY.  
 XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL03900.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 genes from Drosophila and for elucidating cell signaling and cell-cell  
 interactions.  
 XX PS Disclosure; SEQ ID NO 6183; 21pp + Sequence Listing; English.  
 XX CC The invention relates to an isolated nucleic acid detection reagent  
 capable of detecting 1000 or more genes from Drosophila. The invention is  
 useful in developmental biology and in elucidating cell signalling and  
 cell-cell interactions in higher eukaryotes for the development of  
 insecticides, therapeutics and pharmaceutical drugs. The invention  
 discloses genomic DNA sequences (ABL0176-ABL3011) expressed DNA  
 sequences (ABL0840-ABL1675) and the encoded proteins (ABB5773-  
 ABB72072). The sequence data for this patent did not form part of the  
 printed specification, but was obtained in electronic format directly  
 from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 XX SQ Sequence 729 AA;

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 AC AAR56496;  
 XX DE Drosophila TATA-binding protein associated factor dTAF1150 protein.  
 DT 25-MAR-2003 (revised)  
 XX KW Drosophila; TATA-binding protein; TBP associated factor; TFIID;  
 DT 23-MAR-1995 (first entry)  
 XX RNA polymerase II; transcription; messenger RNA; nuclear fraction;  
 DE TATA-binding protein-associated factor dTAF150.  
 XX KW holoenzyme; lambda-gt11; expression library.  
 KW TATA-binding protein associated factor; dTAF150; screening; diagnostic;  
 KW therapeutic; gene transcription regulation.  
 OS Drosophila.  
 XX OS Drosophila.  
 XX OS Drosophila.  
 FH location/Qualifiers  
 FT Key  
 Misc-difference 923  
 /note= "Val or Leu"  
 FT Misc-difference 1106  
 /note= "Arg, Pro or His"  
 FT Misc-difference 1172  
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 FT Misc-difference 1176  
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 XX PN US5314410-A.  
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 PD 09-TUL-1996.  
 XX PP 28-JAN-1994; 94US-00188582.  
 XX PR 28-JUN-1993; 93US-00013412.  
 PR 30-JUN-1993; 93US-00087119.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Comai L, Hoey T, Tanese N, Ruppert S, Weinzierl ROJ, Tjian R,  
 PI Wang E, Dynlacht BD;  
 XX DR WPI; 1996-333245/33.  
 XX DR N-PDBB; AAT42219.  
 XX PT Screen for cpds. that bind human TATA-binding protein associated factor -  
 PT by testing ability to bind to polypeptide fragments of the factor, useful  
 as (ant)agonists of transcription factors involved in disease.  
 XX PS Example; Col 123-132; 86pp; English.  
 XX CC This is the amino acid sequence of the Drosophila TATA-binding protein  
 CC (TBP) associated factor (TAF) designated TAF1150. The protein is a  
 component of the TFIID fraction required for reconstituting RNA  
 polymerase II in vitro transcription activity. The encoded protein has an  
 estimated mol. wt. of 60 kd by SDS-PAGE. The invention relates to  
 CC purified proteins involved in transcription by RNA polymerase II, the RNA  
 polymerase which transcribes messenger RNA. RNA polymerase II  
 CC transcription proceeds in vitro upon addition of several nuclear  
 CC fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II  
 CC holoenzyme. Fraction TFIID has been shown to contains a TBP and other  
 CC TAFs. Purification of TFIID and separation of its components reveals 7  
 CC proteins ranging in size from 30-250 kd. Serum raised against the TFIID  
 CC fraction allowed cloning of the correponding genes from lambda-gt11  
 CC expression libraries. (Updated on 25-MAR-2003 to correct PF field.)  
 XX SQ Sequence 1189 AA;  
 Query Match 54.8%; Score 46; DB 2; Length 1189;  
 Best Local Similarity 53.3%; Pred. No. 2e+02;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LKAMDPPTPPWIKTE 15  
 DB 589 LSAMDSPVILWRLD 603  
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 ID AAW06086  
 ID AAW06086 standard; protein; 1213 AA.  
 AC AAW06086;  
 AC AAW06086;  
 DT 25-MAR-2003 (revised)  
 DT 27-JAN-1997 (first entry)

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XX DE Drosophila TATA-binding protein associated factor dTAF1150 protein.  
 XX KW Drosophila; TATA-binding protein; TBP associated factor; TFIID;  
 XX RNA polymerase II; transcription; messenger RNA; nuclear fraction;  
 DE TATA-binding protein-associated factor dTAF150.  
 XX KW holoenzyme; lambda-gt11; expression library.  
 KW TATA-binding protein associated factor; dTAF150; screening; diagnostic;  
 KW therapeutic; gene transcription regulation.  
 OS Drosophila melanogaster.  
 XX OS Drosophila melanogaster.  
 XX PN US5314410-A.  
 PD 09-TUL-1996.  
 XX PP 28-JAN-1994; 94US-00188582.  
 XX PR 28-JUN-1993; 93US-00013412.  
 PR 30-JUN-1993; 93US-00087119.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Comai L, Hoey T, Tanese N, Ruppert S, Weinzierl ROJ, Tjian R,  
 PI Wang E, Dynlacht BD;  
 XX DR WPI; 1996-333245/33.  
 XX DR N-PDBB; AAT42219.  
 XX PT Screen for cpds. that bind human TATA-binding protein associated factor -  
 PT by testing ability to bind to polypeptide fragments of the factor, useful  
 as (ant)agonists of transcription factors involved in disease.  
 XX PS Example; Col 123-132; 86pp; English.  
 XX CC This is the amino acid sequence of the Drosophila TATA-binding protein  
 CC (TBP) associated factor (TAF) designated TAF1150. The protein is a  
 component of the TFIID fraction required for reconstituting RNA  
 polymerase II in vitro transcription activity. The encoded protein has an  
 estimated mol. wt. of 60 kd by SDS-PAGE. The invention relates to  
 CC purified proteins involved in transcription by RNA polymerase II, the RNA  
 polymerase which transcribes messenger RNA. RNA polymerase II  
 CC transcription proceeds in vitro upon addition of several nuclear  
 CC fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II  
 CC holoenzyme. Fraction TFIID has been shown to contains a TBP and other  
 CC TAFs. Purification of TFIID and separation of its components reveals 7  
 CC proteins ranging in size from 30-250 kd. Serum raised against the TFIID  
 CC fraction allowed cloning of the correponding genes from lambda-gt11  
 CC expression libraries. (Updated on 25-MAR-2003 to correct PF field.)  
 XX SQ Sequence 1213 AA;  
 Query Match 54.8%; Score 46; DB 2; Length 1213;  
 Best Local Similarity 53.3%; Pred. No. 2.1e+02;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LKAMDPPTPPWIKTE 15  
 DB 620 LSAMDSPVILWRLD 634  
 Search completed: January 6, 2005, 10:22:47  
 Job time : 122.189 sec

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## OM protein - protein search, using SW model

Run on: January 6, 2005, 10:23:04 ; Search time 101.351 Seconds  
 (without alignments)  
 53.365 Million cell updates/sec

Title: US-10-047-945-2

Perfect score: 84

Sequence: 1 LKAMDPTPPLWIKTE 15

Scoring table: BIOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4: /cgm2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
6: /cgm2_6/ptodata/1/pubpaa/UCUUS_PUBCOMB.pep:*
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SUMMARIES

RESULT 1

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US-10-047-945-2
; Sequence 2, Application US/10047945
; Publication No. US2003015755A1
; GENERAL INFORMATION:
; APPLICANT: LIPPS, FREDRICK W.
; INVENTOR: LISS, BINIE V.
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENT FOR IMMUNOGLOBULIN B
; TITLE OF INVENTION: (19) IMPLICATED DISORDERS
; FILE REFERENCE: F1M1PA1015US
; CURRENT APPLICATION NUMBER: US/10/047-945
; CURRENT FILING DATE: 2002-01-14
; PRIORITY APPLICATION NUMBER:
; PRIORITY FILING DATE:
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS
; SEQ ID NO: 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM
; OTHER INFORMATION: US 5,576,297.
US-10-047-945-2

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ALIGNMENTS

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2	69	82.1	12	14	US-10-047-945-4	Sequence 4, Appli			Sequence 287756,
3	77.4	11	14	US-10-047-945-5	Sequence 5, Appli			Sequence 255201,	
4	64.3	10	14	US-10-047-945-1	Sequence 1, Appli			Sequence 151167,	
5	50	59.5	9	14	US-10-047-945-6	Sequence 6, Appli			Sequence 205702,
6	59.5	73	17	US-10-047-945-17	Sequence 223175,				Sequence 303133,
7	47	56.0	53.1	15	US-10-047-945-104	Sequence 104, APP			Sequence 257569,
8	46	54.8	85	15	US-10-047-945-278038	Sequence 28038,			Sequence 257580,
9	46	54.8	103	17	US-10-047-945-278038	Sequence 228625,	QY	1 LKAMDPTPPLWIKTE 15	Sequence 8506, AP
10	46	54.8	384	16	US-10-047-945-200494	Sequence 200494,			Sequence 63058, A
11	45	53.6	41	15	US-10-047-945-173148	Sequence 113148,			Sequence 283741,
12	45	53.6	312	10	US-09-883-3034-16	Sequence 16, APP			Sequence 228, APP
13	44	52.4	37	9	US-09-864-761-45321	Sequence 45321, A			Sequence 51474, A

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1	44	52.4	70	15	US-10-424-599-229035	Sequence 229035,			Sequence 229035,
15	44	52.4	95	17	US-10-425-15-237756	Sequence 287756,			Sequence 287756,
16	44	52.4	106	15	US-10-424-599-255201	Sequence 255201,			Sequence 255201,
17	44	52.4	124	15	US-10-424-599-151167	Sequence 151167,			Sequence 151167,
18	44	52.4	144	15	US-10-424-599-205702	Sequence 205702,			Sequence 205702,
19	44	52.4	150	17	US-10-425-115-303133	Sequence 303133,			Sequence 303133,
20	44	52.4	151	17	US-10-425-115-237569	Sequence 257569,			Sequence 257569,
21	44	52.4	151	17	US-10-425-115-257580	Sequence 257580,			Sequence 257580,
22	44	52.4	156	17	US-10-379-930-8506	Sequence 8506, AP			Sequence 8506, AP
23	44	52.4	158	15	US-10-425-114-63058	Sequence 63058, A			Sequence 63058, A
24	44	52.4	153	15	US-10-424-599-233741	Sequence 283741,			Sequence 283741,
25	44	52.4	1336	14	US-10-427-933-228	Sequence 228, APP			Sequence 228, APP
26	43	51.2	8	14	US-10-427-945-7	Sequence 7, APP			Sequence 7, APP
27	43	51.2	68	17	US-10-425-115-251177	Sequence 251177,			Sequence 251177,
28	43	51.2	115	17	US-10-425-115-322493	Sequence 322493,			Sequence 322493,
29	43	51.2	129	17	US-10-437-963-168841	Sequence 168841,			Sequence 168841,
30	43	51.2	156	16	US-10-437-963-114167	Sequence 114167,			Sequence 114167,
31	43	51.2	258	16	US-10-437-963-197262	Sequence 197262,			Sequence 197262,
32	43	51.2	278	16	US-10-437-963-197265	Sequence 197265,			Sequence 197265,
33	43	51.2	286	15	US-10-282-122A-51474	Sequence 51474, A			Sequence 51474, A
34	43	51.2	341	15	US-10-282-122A-73022	Sequence 73022, A			Sequence 73022, A
35	43	51.2	341	15	US-10-282-122A-73158	Sequence 73158, A			Sequence 73158, A
36	43	51.2	341	15	US-10-282-122A-75894	Sequence 144200,			Sequence 144200,
37	43	51.2	840	16	US-10-437-963-144200	Sequence 220, APP			Sequence 220, APP
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42	42	50.0	117	17	US-10-767-701-5623	Sequence 202626,			Sequence 202626,
43	42	50.0	136	17	US-10-425-115-205626	Sequence 228366,			Sequence 228366,
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; Sequence 4, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; FILE REFERENCE: FWLPA1015US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIORITY FILING DATE:  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
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; NUMBER OF SEQ ID NOS: 7  
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; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.

US-10-047-945-4

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Matches 12; Conservative 0; MisMatches 0; Del 0; Insert 0; Other 0;  
Qy 1 LKAMDPTPPW1 12  
Db 1 LKAMDPTPPW1 12

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; Sequence 5, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; FILE REFERENCE: FWLPA1015US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIORITY FILING DATE:  
; SEQ ID NO 5  
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; TYPE: PRT  
; PRIORITY FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
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; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
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US-10-047-945-5

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US-10-047-945-1  
; Sequence 1, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:

Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; FILE REFERENCE: FWLPA1015US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIORITY FILING DATE:  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: SYNTHESIZED. ACTIVE FRAGMENT OF ISOLATE FROM OPOSSUM  
; OTHER INFORMATION: US 5,576,297.  
US-10-047-945-1

Query Match 64.3%; Score 54; DB 14; Length 10;  
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RESULT 5  
US-10-047-945-6  
; Sequence 6, Application US/10047945  
; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, BINIE V.  
; APPLICANT: LIPPS, BINIE V.  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN E  
; FILE REFERENCE: FWLPA1015US  
; CURRENT APPLICATION NUMBER: US/10/047,945  
; CURRENT FILING DATE: 2002-01-14  
; PRIORITY FILING DATE:  
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; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-9 of 2 above.

US-10-047-945-6

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Db 1 LKAMDPTPP 9

RESULT 6  
US-10-422-115-223175  
; Sequence 223175, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.  
 APPLICANT: Kovacic, David K.  
 APPLICANT: Cao, Yongwei  
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 FILE REFERENCE: 38-21(5322)B  
 CURRENT APPLICATION NUMBER: US/10/425,115  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 369326  
 SEQ ID NO 223175  
 LENGTH: 73  
 TYPE: PRT  
 ORGANISM: Zea mays  
 FEATURE:  
 OTHER INFORMATION: Clone ID: MRT4577\_135126C.1.pep  
 US-10-425-115-223175  
 Query Match 59.5%; Score 50; DB 17; Length 73;  
 Best Local Similarity 53.3%; Pred. No. 6.1;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 LKAMDPTPPLWIKTE 15  
 Db 51 LAGIDPDKRGIWIKTE 65  
 RESULT 7  
 US-10-236-417-104  
 Sequence 104, Application US/10236417  
 Publication No.US20040048256A1  
 GENERAL INFORMATION:  
 APPLICANT: Agee et al.  
 TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 FILE REFERENCE: 21402-442C  
 CURRENT APPLICATION NUMBER: US/10/236,417  
 PRIOR APPLICATION NUMBER: US60/318,120  
 PRIOR FILING DATE: 2003-01-06  
 PRIOR FILING DATE: 2001-09-01  
 PRIOR APPLICATION NUMBER: US60/318,430  
 PRIOR FILING DATE: 2001-09-10  
 PRIOR APPLICATION NUMBER: US60/322,781  
 PRIOR FILING DATE: 2001-09-17  
 PRIOR APPLICATION NUMBER: US60/318,184  
 PRIOR FILING DATE: 2001-09-07  
 PRIOR APPLICATION NUMBER: US60/361,663  
 PRIOR FILING DATE: 2002-03-05  
 PRIOR APPLICATION NUMBER: US60/395,412  
 PRIOR FILING DATE: 2002-07-17  
 PRIOR APPLICATION NUMBER: US60/322,636  
 PRIOR FILING DATE: 2001-09-17  
 PRIOR APPLICATION NUMBER: US60/322,817  
 PRIOR FILING DATE: 2001-09-17  
 PRIOR APPLICATION NUMBER: US60/322,816  
 PRIOR FILING DATE: 2001-09-17  
 PRIOR APPLICATION NUMBER: US60/323,519  
 PRIOR FILING DATE: 2001-09-19  
 Remaining Prior Application data removed - See File Wrapper or PAIR.  
 NUMBER OF SEQ ID NOS: 341  
 SOFTWARE: Custom  
 SEQ ID NO 104  
 LENGTH: 531  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-236-417-104  
 Query Match 56.0%; Score 47; DB 15; Length 531;  
 Best Local Similarity 66.7%; Pred. No. 1.1e-02; Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 4 MDPTPPLWIKTE 15  
 Db 70 MDTSPPPLWIKTE 81  
 RESULT 8  
 US-10-424-599-278038  
 Sequence 278038, Application US/10424599  
 Publication No. US20040031072A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa Thomas J  
 APPLICANT: Kovacic David K  
 APPLICANT: Cao Yongwei  
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 FILE REFERENCE: 38-21(5322)B  
 CURRENT APPLICATION NUMBER: US/10/424,599  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 285684  
 SEQ ID NO 278038  
 LENGTH: 85  
 TYPE: PRT  
 ORGANISM: Glycine max  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT3847\_93091C.1.pep  
 US-10-424-599-278038  
 Query Match 54.8%; Score 46; DB 15; Length 85;  
 Best Local Similarity 77.8%; Pred. No. 28;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 7 TPPPLWIKTE 15  
 Db 45 TPPPLWIKTE 53  
 RESULT 9  
 US-10-425-115-228625  
 Sequence 228625, Application US/10425115  
 Publication No. US20040214272A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa, Thomas J.  
 APPLICANT: Kovacic, David K.  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 FILE REFERENCE: 38-21(5322)B  
 CURRENT APPLICATION NUMBER: US/10/425,115  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 369326  
 SEQ ID NO 228625  
 LENGTH: 103  
 TYPE: PRT  
 ORGANISM: Zea mays  
 FEATURE:  
 OTHER INFORMATION: Clone ID: MRT4577\_140098C.1.pep  
 US-10-425-115-228625  
 Query Match 54.8%; Score 46; DB 17; Length 103;  
 Best Local Similarity 87.5%; Pred. No. 33;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 TPPPLWIKT 14  
 Db 50 TPPMWIKT 57  
 RESULT 10  
 US-10-437-963-200494  
 Sequence 200494, Application US/10437963  
 Publication No. US2004123343A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa, Thomas J.  
 APPLICANT: Kovacic, David K.

```

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barnazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US10/437,963
; CURRENT FILING DATE: 2003-05-14
; SEQ ID NO: 200494
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95958C.1.pep
; US-10-437-963-200494

Query Match      54.8%; Score 46; DB 16; Length 384;
Best Local Similarity 58.3%; Pred. No. 1.2e+02; Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY          3 AMDPDPPLWIKT 14
Db          91 AAAPAPPLWLWT 102

RESULT 11
US-10-424-599-173148
; Sequence 173148, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 173148
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_127369C.1.pep
; US-10-424-599-173148

Query Match      53.6%; Score 45; DB 15; Length 41;
Best Local Similarity 63.6%; Pred. No. 19; Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY          5 DPTPPLWIKT 15
Db          14 DPPIPPLWADPE 24

RESULT 12
US-09-885-303A-16
; Sequence 16, Application US/09885303A
; Publication No. US20030032078A1
; GENERAL INFORMATION:
; APPLICANT: TRAVIS, GABRIEL H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF MACULAR
; TITLE OF INVENTION: AND RETINAL DEGENERATIONS
; FILE REFERENCE: UTSD-758US
; CURRENT APPLICATION NUMBER: US/09/885,303A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SEQ ID NO 45321
; LENGTH: 37
; TYPE: PRT

; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-885-303A-16

Query Match      53.6%; Score 45; DB 10; Length 312;
Best Local Similarity 57.1%; Pred. No. 1.4e+02; Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY          1 LKAMDPPTPPIWKI 14
Db          268 LKAMDPSSGLVRT 281

RESULT 13
US-09-864-761-45321
; Sequence 45321, Application US/09864761
; Patent No. US20030048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/698,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SEQ ID NO 45321
; LENGTH: 37
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALI133458.11
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
; OTHER INFORMATION: SWISSPROT HIT: OS3951, EVALU 6.4e+00
; OTHER INFORMATION: EST_HUMAN HIT: AI986481.1, EVALU 6.00e-16
; US-09-864-761-45321

Query Match      52.4%; Score 44; DB 17; Length 95;
Best Local Similarity 66.7%; Pred. No. 61; Matches 6;保守性 2; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          2 KAMDPPTPLWIKT 14
QY          5 KSNGPAPERWMRS 17
Db

RESULT 14
US-10-424-599-229035
; Sequence 229035, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21-(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 229035
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_48845C.1.pep
US-10-424-599-229035

Query Match      52.4%; Score 44; DB 15; Length 70;
Best Local Similarity 60.0%; Pred. No. 45; Matches 9;保守性 0; Mismatches 6; Indels 0; Gaps 0;
QY          1 LKAKDQPKFWIKTE 15
QY          55 LKAKDQPKFWIKTE 69
Db

RESULT 15
US-10-425-115-287756
; Sequence 287756, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21-(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 287756
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_25528C.1.pep
US-10-425-115-287756

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## OM protein - protein search, using sw model

Run on: January 6, 2005, 10:09:51 ; Search time 30.4054 seconds  
 (without alignments) updates/sec  
 32.717 Million cell

Title: US-10-047-945-2  
 Perfect score: 84

Sequence: 1 LKAMDPPTPLWIKR 15

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 45 summaries

Database : Issued\_Parents\_AH:  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*\*  
 3: /cgn2\_5/ptodata/1/iaa/6A\_COMB.pep:\*\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	84	100.0	15 1	US-08-310-340A-1 Sequence 1, Appli
2	84	100.0	15 1	US-08-310-340A-1 Sequence 2, Appli
3	54	64.3	10 1	US-08-657-163A-2 Sequence 1, Appli
4	46	54.8	1213 1	US-08-188-582-20 Sequence 20, Appli
5	46	54.8	1213 1	US-08-641-151-20 Sequence 20, Appli
6	45	53.6	137 4	US-08-134-000-5938 Sequence 5938, Appli
7	42	50.0	910 4	US-10-140-002-112 Sequence 112, Appli
8	41	48.8	151 4	US-09-732-210-1367 Sequence 1367, Appli
9	41	48.8	212 4	US-10-140-002-482 Sequence 482, Appli
10	41	48.8	253 4	US-03-270-767-43223 Sequence 43223, Appli
11	41	48.8	4928 3	US-09-031-9870-5 Sequence 5, Appli
12	41	48.8	4928 3	US-09-370-700-5 Sequence 5, Appli
13	41	48.8	4928 4	US-03-603-207-5 Sequence 5, Appli
14	40	47.6	151 4	US-09-732-210-1353 Sequence 1353, Appli
15	40	47.6	198 4	US-09-270-767-57545 Sequence 57545, Appli
16	40	47.6	303 4	US-03-270-767-42501 Sequence 42501, Appli
17	40	47.6	356 4	US-03-270-767-4479 Sequence 4479, Appli
18	40	47.6	350 4	US-09-020-767-42265 Sequence 42265, Appli
19	39.5	47.0	607 2	US-03-878-989-15 Sequence 15, Appli
20	39.5	47.0	607 3	US-03-272-796-15 Sequence 15, Appli
21	39	46.4	98 2	US-09-047-125-15 Sequence 15, Appli
22	39	46.4	98 3	US-07-736-335B-15 Sequence 15, Appli
23	39	46.4	189 4	US-03-710-279-1998 Sequence 18, Appli
24	39	46.4	205 2	US-08-477-396A-18 Sequence 18, Appli
25	39	46.4	210 4	US-03-270-767-45215 Sequence 45215, Appli
26	39	46.4	228 4	US-03-710-279-1166 Sequence 1166, Appli
27	39	46.4	285 4	US-09-248-796A-20923 Sequence 20923, A

## ALIGNMENTS

RESULT 1  
 US-08-310-340A-1  
 Sequence 1, Application US/08310340A  
 Patent No. 5576297  
 GENERAL INFORMATION:  
 APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND SYNTHETIC LETHAL TOXIN NEUTRALIZING FACTORS AND THEIR TREATMENT FOR ENVENOMATION  
 TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.  
 CITY: BELLAIRE  
 STATE: TEXAS  
 COUNTRY: USA  
 ZIP: 77401  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 5" FLOPPY DISK, 1.44 MB  
 COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/310,340A  
 FILING DATE: 22 SEPTEMBER 1994  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/058, 387  
 FILING DATE: 10 MAY 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME:  
 REGISTRATION NUMBER:  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713-723-6845  
 TELEFAX: 713-663-7290  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQENCE CHARACTERISTICS:  
 LENGTH: 15  
 TYPE: AMINO ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N  
 ORIGINAL SOURCE: OPOSSUM SERA: SEQ ID NO: 1:  
 ORGANISM: DIDELPHIS VIRGINIANA  
 STRAIN: WILD

INDIVIDUAL ISOLATE: TEXAS WILD  
 DEVELOPMENTAL STAGE: ADULT  
 HAPLOTYPE:  
 TISSUE TYPE: BLOOD  
 CELL TYPE:  
 ORGANELLE:

IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1;  
 LIBRARY:  
 CLONE:  
 PUBLICATION INFORMATION:  
 AUTHORS: JONAS PERALES ET AL.  
 TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE  
 JOURNAL: INTERNATIONAL SOCIETY ON  
 TOXICOLOGY  
 VOLUME: 10TH WORLD CONGRESS ON ANIMAL  
 PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,  
 ISSUE: PROGRAMME AND ABSTRACTS  
 PAGES: 104  
 DATE: 3-8 NOV 1991

S-08-310-340A-1

RESULT 2  
 US-08-657-163A-1  
 Query Match 100.0%; score 84; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
 SYNTHETIC LTNFS AND THEIR  
 TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 NUMBER OF SEQUENCES: 3  
 CURRENT APPLICATION DATA:  
 ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.  
 CITY: BELLAIRE  
 STATE: TEXAS  
 COUNTRY: USA  
 ZIP: 77401  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB  
 COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/657,163A  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/310,340  
 FILING DATE: 22 SEPTEMBER 1994  
 CLASSIFICATION: 514  
 APPLICATION NUMBER: 08/058,387  
 FILING DATE: 10 MAY 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JOHN R. CASPERSON  
 REGISTRATION NUMBER: 28,198  
 REFERENCE/DOCKET NUMBER: FML-PAT-US-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713-663-7290  
 TELEFAX: 713-492-2961  
 INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 15  
 TYPE: AMINO ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N  
 ORIGINAL SOURCE: OPOSSUM SERA; SEQ ID NO: 1;  
 ORGANISM: DIDELPHIS VIRGINIANA  
 STRAIN: WILD  
 INDIVIDUAL ISOLATE: TEXAS WILD  
 DEVELOPMENTAL STAGE: ADULT  
 HAPLOTYPE: BLOOD  
 TISSUE TYPE: BLOOD  
 CELL TYPE:  
 ORGANELLE:

IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1;  
 LIBRARY:  
 CLONE:  
 PUBLICATION INFORMATION:  
 AUTHORS: JONAS PERALES ET AL.  
 TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE  
 JOURNAL: INTERNATIONAL SOCIETY ON  
 TOXICOLOGY  
 VOLUME: 10TH WORLD CONGRESS ON ANIMAL  
 PLANT AND MICROBIAL TOXINS 3-8 NOV 1991, SINGAPORE  
 ISSUE: PROGRAMME AND ABSTRACTS  
 PAGES: 104  
 DATE: 3-8 NOV 1991

US-08-657-163A-1

RESULT 3  
 US-08-657-163A-2  
 Query Match 100.0%; Score 84; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0;  
 Qy 1 LKAMDPTPPLWIKTE 15  
 Db 1 LKAMDPTPPLWIKTE 15  
 CURRENT APPLICATION DATA:  
 ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.  
 CITY: BELLAIRE  
 STATE: TEXAS  
 COUNTRY: USA  
 ZIP: 77401  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB  
 COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/657,163A  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/310,340  
 FILING DATE: 22 SEPTEMBER 1994  
 CLASSIFICATION: 514  
 APPLICATION NUMBER: 08/058,387  
 FILING DATE: 10 MAY 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JOHN R. CASPERSON  
 REGISTRATION NUMBER: 28,198  
 REFERENCE/DOCKET NUMBER: FML-PAT-US-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713-663-7290  
 TELEFAX: 713-492-2961  
 INFORMATION FOR SEQ ID NO: 1:

APPLICATION NUMBER: 08/188,582,387  
 FILING DATE: 10 MAY 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JOHN R. CASPERSON  
 REGISTRATION NUMBER: 28,198  
 REFERENCE/DOCKET NUMBER: FWL-PAT-US-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 713-462-2961  
 TELEFAX: 713-663-7290  
 TELX:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10  
 TYPE: AMINO ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N  
 ORIGINAL SOURCE: SYNTHETIC  
 IS-08-657-163A-2  
 RESULT 4  
 Query Match 64.3%; Score 54; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.029; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 GENERAL INFORMATION:  
 Sequence 20, Application US/08188582  
 Patent No. 553410  
 APPLICANT: Tjian, Robert  
 APPLICANT: Comai, Lucio  
 APPLICANT: Dynlact, Brian D.  
 APPLICANT: Hoey, Timothy  
 APPLICANT: Ruppert, Siegfried  
 APPLICANT: Tanese, Naoko  
 APPLICANT: Wang, Edith  
 APPLICANT: Weinzierl, Robert O.J.  
 TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FLERH, HOHBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,715  
 FILING DATE: 09-MAY-1996  
 CLASSIFICATION: 45  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/188,582  
 FILING DATE: 28-JAN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Osman, Richard A.  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: A-57650-2/AUT/RAO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELX: 910 277299  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1213 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-188-582-20  
 RESULT 5  
 Query Match 54.8%; Score 46; DB 1; Length 1213;  
 Best Local Similarity 53.3%; Pred. No. 69;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Db 620 LSAMDSPVWIRLD 634  
 GENERAL INFORMATION:  
 Patent No. 5637686  
 APPLICANT: Tjian, Robert  
 APPLICANT: Comai, Lucio  
 APPLICANT: Dynlact, Brian D.  
 APPLICANT: Hoey, Timothy  
 APPLICANT: Ruppert, Siegfried  
 APPLICANT: Tanese, Naoko  
 APPLICANT: Wang, Edith  
 APPLICANT: Weinzierl, Robert O.J.  
 TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FLERH, HOHBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 08/188,582  
 FILING DATE: 28-JAN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Osman, Richard A.  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: A-57650-2/AUT/RAO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELX: 910 277299  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1213 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-646-715-20  
 Query Match 54.8%; Score 46; DB 1; Length 1213;  
 Best Local Similarity 53.3%; Pred. No. 69;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 620 LSAMDSPVWIRLD 634

RESULT 6  
US-09-134-000C-5938  
; Sequence 5938, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032795-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5938  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis

US-09-134-000C-5938

Query Match Score 45; DB 4; Length 137;  
Best Local Similarity 75.0%; Pred. No. 10;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DPTPLW1 12  
Db 85 NPTPLWV 92

RESULT 7  
US-10-140-002-112  
; Sequence 112, Application US/10140002  
; Patent No. 6725730  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desorge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanaabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACTDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C59  
; CURRENT APPLICATION NUMBER: US/10/140,002  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 112  
; LENGTH: 910  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-140-002-112

Query Match Score 42; DB 4; Length 910;  
Best Local Similarity 46.7%; Pred. No. 2.1e+02;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LKAMDPPLWIKTE 15

---

Db 506 IECVDPTEPHNDE 520

RESULT 8  
US-09-732-210-1367  
; Sequence 1367, Application US/09732210  
; Patent No. 6573361  
; GENERAL INFORMATION:  
; APPLICANT: Bunkers, Greg J.  
; APPLICANT: Liang, Jihong  
; APPLICANT: Mittanck, Cindy A.  
; APPLICANT: Seal, Jeffrey W.  
; APPLICANT: Wu, Yonne S.  
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use  
; FILE REFERENCE: 38-21(1503)B  
; CURRENT APPLICATION NUMBER: US/09/732,210  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,513  
; PRIOR FILING DATE: 1999-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,340  
; NUMBER OF SEQ ID NOS: 1753  
; SEQ ID NO 1367  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Zea mays

US-09-732-210-1367

Query Match Score 41; DB 4; Length 151;  
Best Local Similarity 75.0%; Pred. No. 46;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TPPLMT 14  
Db 21 TPPTWKT 28

RESULT 9  
US-10-140-002-482  
; Sequence 482, Application US/10140002  
; Patent No. 6725730  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desorge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanaabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACTDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C59  
; CURRENT APPLICATION NUMBER: US/10/140,002  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 482  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-140-002-482

Query Match 48.8%; Score 41; DB 4; Length 212;  
 Best Local Similarity 66.7%; Pred. No. 66;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 MDPPRPIWI 12  
 Db 136 MDPSVPIWI 144

RESULT 10  
 US-09-270-767-43223  
 Sequence 43223, Application US/09270767  
 Patent No. 6703491  
 GENERAL INFORMATION:  
 APPLICANT: Homburger et al.  
 TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 FILE REFERENCE: File Reference: 7326-094  
 CURRENT APPLICATION NUMBER: US/09/270,767  
 CURRENT FILING DATE: 1999-03-17  
 NUMBER OF SEQ ID NOS: 6251.0  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 43223  
 LENGTH: 253  
 TYPE: PRT  
 ORGANISM: *Drosophila melanogaster*  
 FEATURE:  
 OTHER INFORMATION: Xaa means any amino acid

Query Match 48.8%; Score 41; DB 4; Length 253;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDPTPPL 10  
 Db 43 MDPRPPL 49

RESULT 11  
 US-09-036-987A-5  
 Sequence 5, Application US/09036987A  
 Patent No. 614525

GENERAL INFORMATION:  
 APPLICANT: Baltz, Richard H.  
 APPLICANT: Broughton, Mary C.  
 APPLICANT: Crawford, Kathryn P.  
 APPLICANT: Madduri, Krishnamurthy  
 APPLICANT: Merlo, Donald J.  
 APPLICANT: Treadaway, Patti J.  
 APPLICANT: Turner, Jan R.  
 APPLICANT: Waldron, Clive  
 APPLICANT: Waldrion, Clive  
 TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
 NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:  
 ADDRESSE: Dow AgroSciences LLC Patent Department  
 STREET: 9130 Zionsville Road  
 CITY: Indianapolis  
 STATE: Indiana  
 COUNTRY: USA  
 ZIP: 46268

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/036, 987A  
 FILING DATE: 09-MAR-1998  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Stuart, Donald R.  
 REGISTRATION NUMBER: 28,479

REFERENCE/DOCKET NUMBER: 50,608  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (317)337-4816  
 TELEX: (317)337-4847

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 4928 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-09-036-987A-5

Query Match 48.8%; Score 41; DB 3; Length 4928;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPPLWIKT 14  
 Db 2850 LRADADVAPLWLAT 2863

RESULT 12  
 US-09-370-700-5  
 Sequence 5, Application US/09370700  
 Patent No. 6273350  
 GENERAL INFORMATION:  
 APPLICANT: Baltz, Richard H.  
 APPLICANT: Broughton, Mary C.  
 APPLICANT: Crawford, Kathryn P.  
 APPLICANT: Madduri, Krishnamurthy  
 APPLICANT: Treadaway, Patti J.  
 APPLICANT: Turner, Jan R.  
 APPLICANT: Waldron, Clive  
 APPLICANT: Waldrion, Clive  
 TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
 CURRENT APPLICATION NUMBER: US/09/370,700  
 CURRENT FILING DATE: 1999-06-09  
 EARLIER APPLICATION NUMBER: US 09/36987  
 EARLIER FILING DATE: 1998-03-09  
 NUMBER OF SEQ ID NOS: 39  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 5  
 LENGTH: 4928  
 TYPE: PRT  
 ORGANISM: *Saccharopolyspora spinosa*

US-09-370-700-5

Query Match 48.8%; Score 41; DB 3; Length 4928;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03; Indels 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPPLWIKT 14  
 Db 2850 LRADADVAPLWLAT 2863

RESULT 13  
 US-09-603-207-5  
 Sequence 5, Application US/09603207B  
 Patent No. 6521405  
 GENERAL INFORMATION:  
 APPLICANT: Baltz, Richard H.  
 APPLICANT: Broughton, Mary C.  
 APPLICANT: Crawford, Kathryn P.  
 APPLICANT: Madduri, Krishnamurthy  
 APPLICANT: Treadaway, Patti J.  
 APPLICANT: Turner, Jan R.  
 APPLICANT: Waldron, Clive  
 TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
 FILE REFERENCE: 5089 DIVI  
 CURRENT APPLICATION NUMBER: US/09/603, 207B  
 CURRENT FILING DATE: 2000-06-23  
 EARLIER APPLICATION NUMBER: 09/370,700

; EARLIER FILING DATE: 1998-03-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 4928

; ORGANISM: Saccharopolyspora spinosa  
; US-09-603-207-5

Query Match 48.8%; Score 41; DB 4; Length 4928;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LKAMDPTPPWIKT 14  
Db 2850 LRADDSAPWILAT 2863

RESULT 14  
US-09-732-210-1353  
; Sequence 1153, Application US/09732210

; Patent No. 6573361  
; GENERAL INFORMATION:  
; APPLICANT: Bunkers, Greg J.  
; APPLICANT: Liang, Jihong  
; APPLICANT: Mittanck, Cindy A.  
; APPLICANT: Seale, Jeffrey W.  
; APPLICANT: Wu, Yonne S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use  
FILE REFERENCE: 38-2-(15036)B  
CURRENT APPLICATION NUMBER: US/09/732,210  
CURRENT FILING DATE: 2000-12-07  
PRIOR APPLICATION NUMBER: US 60/169,513  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: US 60/169,340  
NUMBER OF SEQ ID NOS: 1753  
SEQ ID NO 1353  
LENGTH: 151

; TYPE: PRY  
; ORGANISM: Agaricus bisporus  
; US-09-732-210-1353

Query Match 47.6%; Score 40; DB 4; Length 151;  
Best Local Similarity 75.0%; Pred. No. 66;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 TPPWIKT 14  
Db 21 TPPSWIKT 28

RESULT 15  
US-09-270-767-57545

; Sequence 57545, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 57545  
LENGTH: 198

; TYPE: PRY  
; ORGANISM: *Drosophila melanogaster*  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
; US-09-270-767-57545

	Best Local Similarity	Pred. No.	Indels	Gaps
QY	54.5%	88	0	0
Db	50.0%	11	0	0

Search completed: January 6, 2005, 10:25:06  
Job time : 31.4054 SECS

Om protein - protein search, using sw model									
Run on: January 6, 2005, 10:09:21 ; Search time 18:8108 Seconds (without alignments) 61.380 Million cell updates/sec									
Title: US-10-047-945-4									
Perfect score: 69									
Sequence: 1 LKAMDPPPLWI 12									
Scoring table: BLOSUM62									
Searched: Gapext 0.5									
Total number of hits satisfying chosen parameters: 283416									
Minimum DB seq length: 0									
Maximum DB seq length: 200000000									
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
Database : PIR 79;*									
1: pir1;*									
2: pir2;*									
3: pir3;*									
4: pir4;*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	% Match Length	DB ID	Description	QY	1 LKAMDPPPLWI 12	Db	1 LKAMDPPPLWI 12	ALIGNMENTS
1	52	75.4	237	A42013					RESULT 1
2	43	62.3	695	B75099					
3	43	62.3	932	A31898					
4	43	62.3	1213	A54063					
5	42	60.9	115	2 DT1194					
6	42	60.9	398	2 A81719					
7	42	60.9	3990	2 C69900					
8	42	60.9	1327	2 T0402					
9	41	59.4	707	2 F89295					
10	41	59.4	967	2 S53360					
11	40	58.0	205	2 S28854					
12	40	58.0	205	2 A10525					
13	40	58.0	225	2 C83867					
14	40	58.0	406	2 T03404					
15	40	58.0	560	2 T03404					
16	40	58.0	609	2 S65208					
17	39.5	57.2	365	2 F87552					
18	39	56.5	268	2 S31010					
19	39	56.5	426	2 T16405					
20	39	56.5	492	2 T16659					
21	39	56.5	564	1 VRHENV					
22	39	56.5	663	1 A65798					
23	39	56.5	1212	2 D88175					
24	39	56.5	1215	2 B70614					
25	39	56.5	1425	2 C88175					
26	39	56.5	1728	2 T1466					
27	38.5	55.8	401	1 REMSK					
28	38.5	55.8	402	1 REMSK					
29	38	55.1	259	2 C71820					

**RESULT 3**

A31898 hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - sea urchin (Strongylocentrotus purpuratus (purple urchin))  
 C;Species: Strongylocentrotus purpuratus (purple urchin)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: A31898; A28367  
 R;Woodward, H.D.; Allen, J.M.C.; Lennarz, W.J.  
 J. Biol. Chem. 263, 18411-18418, 1988  
 A;Title: 3-hydroxy-3-methylglutaryl-coenzyme A reductase of the sea urchin embryo. Deduced  
 A;Reference number: A31898; MUID:9054023; PMID:192541  
 A;Accession: A31898  
 A;Molecule type: mRNA  
 A;Residues: 1-932 <WOO>  
 A;Cross-references: UNIPROT:PI6393; GB:J04200; NID:9161522; PIDN:AAA3060\_1; PID:9161523  
 A;Note: the authors translated the codon GGA for residue 805 as Glu  
 Submitted to GenBank  
 Best Local Similarity 62.3%; Score 43; DB 1; Length 932;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 KAMDPPTPPLW 11  
 Db 298 KRKIDPTPMLW 307

**RESULT 4**

A54063 TATA-binding protein-associated factor II - fruit fly (Drosophila melanogaster)  
 C;Species: Drosophila melanogaster  
 C;Date: 02-Aug-1994 #sequence\_revision 02-Aug-1994 #text\_change 09-Jul-2004  
 C;Accession: A54063  
 R;Verrijzer, C.P.; Yokomori, K.; Chen, J.L.; Tjian, R.  
 Science 264, 933-941, 1994  
 A;Title: Drosophila TAF-II 150: similarity to yeast gene TSM-1 and specific binding to DNA  
 A;Reference number: A54063; MUID:94233377; PMID:8178153  
 A;Status: preliminary; not compared with conceptual translation  
 A;Residues: 1-1213 <VER>  
 A;Cross-references: UNIPROT:024325; GB:X79243; NID:9541664; PIDN:CAA55830\_1; PID:9541665  
 A;Gene: FlyBase:raf150  
 A;Cross-references: FlyBase:FBgn0011836

Query Match 62.3%; Score 43; DB 2; Length 1213;  
 Best Local Similarity 66.7%; Pred. No. 52;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ||||| : ||||| LKAMDPPTPPLW 12  
 Db 620 LSAMDSPPLW 631

**RESULT 5**

D71194 hypothetical protein PH1828 - Pyrococcus horikoshii  
 C;Species: Pyrococcus horikoshii  
 C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004

**RESULT 6**

A81717 conserved hypothetical protein TC0306 [imported] - Chlamydia muridarum (strain Nigg)  
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoN  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C;Accession: A81717  
 R;Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.; Nucleic Acids Res. 28, 1397-1406, 2000  
 A;Title: Genome sequences of Chlamydia trachomatis MoN and Chlamydia pneumoniae AR39.  
 A;Reference number: A81500; MUID:2010255; PMID:1064935  
 A;Accession: A81717  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-398 <TET>  
 A;Cross-references: UNIPROT:O9PLO2; GB:AE002298; GB:AE002160; NID:97190343; PIDN:AAF3917  
 A;Experimental source: strain Nigg (MoN)  
 C;Genetics:  
 A;Gene: TC0306  
 C;Superfamily: Chlamydia trachomatis hypothetical protein CT0306  

Query Match 60.9%; Score 42; DB 2; Length 398;  
 Best Local Similarity 77.8%; Pred. No. 22;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 KAMDPPTPPL 10  
 Db 309 KEKDPTPPL 317

**RESULT 7**

A22900 fasciclin I precursor - American bird grasshopper  
 C;Species: Schistocerca americana (American bird grasshopper)  
 C;Date: 22-Aug-1988 #sequence\_revision 22-Aug-1988 #text\_change 09-Jul-2004  
 C;Accession: A22900; A31817  
 R;Zinn, K.; McAllister, L.; Goodman, C.S.  
 Cell 53, 577-587, 1988  
 A;Title: Sequence analysis and neuronal expression of fasciclin I in grasshopper and Drosophila  
 A;Reference number: A22900; MUID:88223351; PMID:3370670  
 A;Accession: A22900  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-662 <ZIN>  
 A;Cross-references: UNIPROT:PI6075; GB:M02544; GB:J03787; NID:9160846; PID:9160847  
 R;Snow, P.M.; Zinn, K.; Harrelson, A.L.; McAllister, L.; Schilling, J.; Bastiani, M.J.; Proc. Natl. Acad. Sci. U.S.A. 85, 5291-5295, 1988  
 A;Title: Characterization and cloning of fasciclin I and fasciclin II glycoproteins in the

A; Reference number: A94202; MUID:88276943; PMID:2839842  
 A; Accession: A31817  
 A; Molecule type: mRNA  
 A; Cross-references: EMBL:M20544; EMBL:J03787

Query Match 60.9%; Score 42; DB 2; Length 662;  
 Best Local Similarity 58.3%; Pred. No. 39;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Ov 1 1 LKAMDPTPPLWI 12  
 Db 104 LSBDGNPPLWI 115

## RESULT 8

T09402

immunoglobulin-like protein IGSF1 - human

C;Species: Homo sapiens (man)

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

R;Mazzarella, R.; Penguin, G.; Jones, J.; Jones, C.; Schlessinger, D.

Genomics 48, 157-162, 1998

A;Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xg25.

A;Reference number: Z16665; MUID:98190514; PMID:9521868

A;Accession: T09402

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1327 &lt;M2&gt;

A;Cross-references: UNIPROT:O15070; EMBL:A034198; NID:92645889; PIDN: AAC52057.1; PID:9456

C;Genetics:

A;Gene: igsf1

A;Map position: xq25

Query Match 60.9%; Score 42; DB 2; Length 1327;  
 Best Local Similarity 58.3%; Pred. No. 84;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Ov 4 MDTPPPPLWI 12  
 Db 25 MDPQPELWI 33

## RESULT 9

T86925

probable acyl-CoA synthetase [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004

C;Accession: P86925

R;Cole, S.T.; Eiglmeier, K.; Parish, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc

ean, M.A.; Rutherford, K.M.

Nature 409, 107-1011, 2001

A;Authors: Butcher, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: P86925

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-707 &lt;STO&gt;

A;Cross-references: UNIPROT:Q9CD82; GB:AL450380; NID:913092512; PIDN:CAC29642.1; GSPDB:G

A;Genetics:

A;Gene: fabD22

Query Match 59.4%; Score 41; DB 2; Length 707;  
 Best Local Similarity 54.5%; Pred. No. 61;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Ov 1 1 LKAMDPTPPLWI 11

Db 486 LRQASPTKPIW 496

## RESULT 10

S58360

lantibiotic Peps5 biosynthesis protein pppB - *Staphylococcus epidermidis*C;Species: *Staphylococcus epidermidis*

C;Date: 14-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C;Accession: S66655; S58360

R;Meyer, C.; Bierbaum, G.; Heidrich, C.; Reis, M.; Sueing, J.; Iglesias-Wind, M.I.; Ken

Bur, J. Biochem. 232, 478-489, 1995

A;Title: Nucleotide sequence of the lantibiotic Peps5 biosynthetic gene cluster and func

A;Reference number: S66651; MUID:96035882; PMID:7556197

A;Accession: S66655

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-957 &lt;STO&gt;

C;Genetics:

A;Gene: pepB

C;Keywords: antibiotic biosynthesis

Query Match 59.4%; Score 41; DB 2; Length 967;

Best Local Similarity 54.5%; Pred. No. 87; Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Ov 1 LKAMDPTPPLWI 11

Db 102 IKALDTNPW 112

## RESULT 11

S26854

microfilarial sheath protein, major component - nematode (*Brugia pahangi*)C;Species: *Brugia pahangi*

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C;Accession: S26854

R;Selkirk, M. submitted to the EMBL Data Library, February 1991

A;Reference number: S26854

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1205 &lt;SEL&gt;

A;Cross-references: UNIPROT:Q00032; EMBL:X58063; NID:95951; PID:95952

C;Genetics:

A;Introns: 123/2

Query Match 58.0%; Score 40; DB 2; Length 205;  
 Best Local Similarity 54.5%; Pred. No. 23; Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Ov 1 LKAMDPTPPLWI 11

Db 146 LTQQTPIPPIN 156

## RESULT 12

A0525

proline-rich sheath protein MF22 precursor - nematode (*Brugia pahangi*)C;Species: *Brugia pahangi*

C;Date: 28-Feb-1992 #sequence\_revision 10-Apr-1992 #text\_change 09-Jul-2004

C;Accession: A40525

R;Selkirk, M.B.; Yazdanbakhsh, M.; Freedman, D.; Blaxter, M.L.; Cookson, B.; Jenkins, R

J. Biol. Chem. 266, 11002-11003, 1991

A;Title: A proline-rich structural protein of the surface sheath of larval *Brugia* filar

A;Reference number: A40525; MUID:91250404; PMID:1710216

A;Accession: A40525

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-205 &lt;SEL&gt;

A;Cross-references: UNIPROT:Q00032; GB:X58063

A;Note: the authors translated the codon GCA for residue 23 as Arg, CTC for residue 146

Query Match 58.0%; Score 40; DB 2; Length 205;

Best Local Similarity 54.5%; Pred. No. 23;

QY  
Db  
6 PTPPLWI 12  
| : | : |  
389 PSPPLWV 399

RESULT 13

RESULT 13  
T02404

C-Species: *Arabidopsis thaliana* "mouse-ear Cress"  
 C-Date: 05-Mar-1999 #Sequence\_revision 05-Mar-1999 #Text\_change 09-Jul-2004  
 C-Accesion: T04404; BB4879  
 R-Rounley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.R.  
 submitted to the EMBL Data Library, May 1998  
 A-Description: *Arabidopsis thaliana* chromosome II BAC F411 genomic sequence.  
 A-Reference number: D4667  
 A-Accesion: T04404

**RESULT** 14  
 C83867  
 Xaa-Pro dipeptidase BH1719 [imported] - *Bacillus halodurans* (strain C-125)  
 C;Species: *Bacillus halodurans*  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C;Accession: C83867  
 R;Takami, H.; Nakagne, K.; Tsakai, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirao, A.;Nucleic Acids Res. 28, 4317-4331, 2000  
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and its physiological properties  
 A;Reference number: A83650; NID:20512502; PMID:11058132  
 A;Accession: C83867  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-406 <STO>  
 A;Cross-references: UNIPROT:Q3KC35; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BA054  
 A;Experimental source: strain C-125  
 C;Genetics:  
 A;Gene: BH1719

Query Match Similarity 58.0%; Score 40; DB 2; Length 406;  
 Best: Local Similarity 71.4%; Pred. No. 49;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 6, 2005, 10:00:35 ; Search time 102.811 Seconds

(without alignments) 67.157 Million cell updates/sec

Title: US-10-047-945-4  
Perfect score: 69  
Sequence: 1 LKAMDPTPPLWI 12

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched:

1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : UniProt\_02;\*

1: uniprot\_sprot;\*

2: uniprot\_trembl;\*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	69	100.0	17	2	Q9TR78 didelphis m
2	69	100.0	291	1	DM43 DIDMR
3	60	87.0	140	2	Q8HZT5 didephisi m
4	60	87.0	291	2	Q8HZT4 didephisi m
5	52	75.4	314	2	Q8HYX5 didephisi m
6	50	72.5	227	2	Q73zb2 mycobacteri
7	46	72.5	227	2	AAS04008
8	46	66.7	370	2	Q7QB48
9	45	65.2	128	2	Q833V1 anophiles g
10	45	65.2	457	2	Q7YQJ7 enterococcus
11	44	63.8	242	2	Q8BXK6
12	44	63.8	477	2	Q81850 caenorhabdi
13	43	62.3	351	1	Y4VJL RHISN
14	43	62.3	354	2	Q8WM74
15	43	62.3	360	2	Q84678 myxococcus
16	43	62.3	695	2	Q9UZG1
17	43	62.3	932	1	HMDH STRPU
18	42	62.3	1221	1	TAF2 DRME
19	42	60.9	115	2	Q59432
20	42	60.9	190	2	Q7Q324
21	42	60.9	242	2	Q8BN6C5
22	42	60.9	355	2	Q6FPB99
23	42	60.9	408	1	Y3306 CHLMU
24	42	60.9	408	2	Q7WLB6
25	42	60.9	576	2	Q6YID6
26	42	60.9	576	2	AN17670
27	42	60.9	576	2	Q83WK7
28	42	60.9	612	2	1 PAS1 SCHAM
29	42	60.9	662	1	P10675 schistocerc
30	42	60.9	1437	2	O15070 homo sapien
31	41	59.4	591	2	Q8FBn0 corvinae
32	41	59.4	32	1	Q6cs847 kluveromyco

RESULT 1

ID	Q9TR78	PRELIMINARY;	PRT;	17 AA.
AC	Q9TR78;			
DT	01-MAY-2000	(TREMBL: 13, Created)		
DT	01-MAY-2000	(TREMBL: 13, Last sequence update)		
DT	01-MAR-2001	(TREMBL: 16, Last annotation update)		
DB	ANTI-BOTHROPIC complex 48,000 SUBUNIT (Fragment).			
OS	Didelphis marsupialis (Southern opossum).			
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Didelphis.			
OX	NEBI_TaxID=9268;			
RN	[1]			

ALIGNMENTS

SEQUENCE	RX	RA	RT	RT	RT	RT	RL	SQ
MEDLINE=95149299; PubMed=7846694; Peralles J., Mousatche H., Marangoni S., Oliveira B., Demont G.B.; Isolation and partial characterization of an anti-bothropic complex from the Berlin of South American Didelphidae.; Toxicon 32:1237-1249(1994); NEBI_TaxID=9268;	RX	RA	RT	RT	RT	RT	RL	SQ
SEQUENCE	17 AA;	1947 MW;	C555FB40E873B2A2A CRC64;					
RESULT 2								
Query	Q9TR78 didelphis m	Match	100.0%; Score 69; DB 2; Length 17;					
Matches	12;	Local Similarity	100.0%; Pred. No. 0.00270;					
Matched	12;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;					
DB	1 LKAMDPTPPLWI 12							
AC	Q9TR78;	ID	DM43 DIDMR	STANDARD;	PRT;	291 AA.		
DT	01-MAR-2001	DT	01-MAR-2001	(Rel. 40, Created)				
DT	28-FEB-2003	DT	05-JUL-2004	(Rel. 41, Last sequence update)				
DT	(Rel. 41, Last sequence update)	DE	(Rel. 44, Last annotation update)					
OS	Didelphis marsupialis (Southern opossum).							
OC	BuKarYota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Metatheria; Didelphimorpha; Didelphidae; Didelphis.							
OX	NEBI_TaxID=9268;							
RN	[1]							

SEQUENCE, AND MASS SPECTROMETRY

RC	RC	RC	RC	RA	RA	RA	RA	RA
TISSUE-Serum;	TISSUE-Serum;	TISSUE-Serum;	TISSUE-Serum;	NEVES-TERREIRA, A.G.C., PEREIRAS J., FOX J.W., SHANNON J.D.,	MAKIN D.L., GARRETT R.C., DOMONT G.B.,			
MEDLINE=21935368; PubMed=18185628; DOI=10.1074/jbc.M200589200;				NEVES-TERREIRA, A.G.C., PEREIRAS J., FOX J.W., SHANNON J.D.,	STRUCTURAL AND FUNCTIONAL ANALYSES OF DM43, A SNAKE VENOM	STRUCTURAL AND FUNCTIONAL ANALYSES OF DM43, A SNAKE VENOM	STRUCTURAL AND FUNCTIONAL ANALYSES OF DM43, A SNAKE VENOM	STRUCTURAL AND FUNCTIONAL ANALYSES OF DM43, A SNAKE VENOM
				NEVES-TERREIRA, A.G.C., PEREIRAS J., FOX J.W., SHANNON J.D.,	METALLOPROTEINASE INHIBITOR FROM Didelphis marsupialis SERUM.;			
					J. Biol. Chem. 277:13129-13137(2002);			
					-I- FUNCTION: Metalloproteinase inhibitor.			
					CC	CC	CC	CC
					-I- SURUNIT: Homodimer.	-I- SURUNIT: Homodimer.	-I- SURUNIT: Homodimer.	-I- SURUNIT: Homodimer.
					SEQUENCE SPECIFICITY: Blood and milk.			

CC -1 PTM: N-glycosylated.  
 CC -1 MASS SPECTROMETRY: MW=42991; METHOD=MALDI; RANGE=1-291;  
 CC NOTE=Ref.1.  
 CC -1 SIMILITY: Contains 3 immunoglobulin-like V-type domains.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR011015; LEM-like.  
 DR Pfam: PF00047; Ig; 1.  
 DR PROSITE; PS50035; Ig\_LIKE; 1.  
 DR Direct protein sequencing; Glycoprotein; Immunoglobulin domain;  
 KW Metalloprotease inhibitor; Repeat.  
 FT DOMAIN 22 79  
 DOMAIN 114 171  
 DOMAIN 191 288  
 DOMAIN 28 74  
 DISULFID 121 163  
 DISULFID 213 265  
 CARBOHYD 23 23  
 CARBOHYD 156 156  
 CARBOHYD 160 160  
 CARBOHYD 175 175  
 SEQUENCE 291 AA; 32390 MW; 17A496227E69A65B CRC64;

Query Match 100.0%; Score 69; DB 1; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 0.056; Pred. 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 12; -

Qy 1 LKAMDPTPPW1 12  
 Db 1 LKAMDPTPPW1 12

RESULT 3  
 Q8HZ75 PRELIMINARY; PRT; 140 AA.  
 ID Q8HZ75  
 AC Q8HZ75;  
 DT 01-MAR-2003 (TREMBIrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREMBIrel. 26, Last annotation update)  
 DE Alpha 1B glycoprotein DWP51-D (Fragment).  
 OS Didelphis marsupialis virginiana (North American opossum).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.  
 OX NCBI\_TAXID=9267;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Martinez M.B.; Pierce J.R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AAV131000; AAN06911.1; -.  
 DR InterPro; IPR011015; LEM\_like.  
 FT NON\_TER 140 140  
 SQ SHQUNCE 140 AA; 15297 MW; E19D071A76AA5A7F CRC64;

Query Match 87.0%; Score 60; DB 2; Length 140;  
 Best Local Similarity 91.7%; Pred. No. 0.075; Pred. 0; Mismatches 1; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPW1 12  
 Db 42 LKAMDPTPPW1 53

RESULT 4  
 Q8HZ74 PRELIMINARY; PRT; 291 AA.  
 ID Q8HZ74  
 AC Q8HZ74;  
 DT 01-MAR-2003 (TREMBIrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREMBIrel. 26, Last annotation update)  
 DB Alpha 1B glycoprotein DWP51-D (Fragment).  
 OS Didelphis marsupialis virginiana (North American opossum).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

OX NCBI\_TAXID=9267;  
 RN [1]\_SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.

RA Domont G.B.; Ho P.L.; Berales J.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY163805; AAN64690.1; -.  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART; SM00403; Ig; 1.  
 DR PROSITE; PS50035; Ig\_LIKE; 1.  
 KW Signal.  
 FT SIGNAL 1 23 Potential.  
 FT CHAIN 24 314 venom metalloproteinase inhibitor DM43b.  
 SQ SEQUENCE 314 AA; 34604 MW; 6D5D55B448D035A5 CRC64;

Query Match 75.4%; Score 52; DB 2; Length 314;  
 Best Local Similarity 83.3%; Pred. No. 3.5; Pred. 0; Mismatches 2; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPW1 12  
 Db 24 LKAMDPTPPW1 35

RESULT 6  
 Q73ZB2 PRELIMINARY; PRT; 227 AA.  
 ID Q73ZB2  
 AC Q73ZB2;  
 DT 05-JUL-2004 (TREMBIrel. 27, Created)  
 DT 05-JUL-2004 (TREMBIrel. 27, Last sequence update)  
 DB Hypothetical protein.  
 GN OrderedLocusNames=MAP1691c;

OS Mycobacterium paratuberculosis.  
 OC Bacteria; Actinobacteria; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;  
 OC Mycobacterium avium complex (MAC).  
 RN NCBI\_TaxID=1770;  
 RP [1] SEQUENCE FROM N.A.  
 RC STRAIN=10;  
 RA Li L., Bannantine J., Zhang Q., Amongsin A., Alt D., Kapur V., Li L., Submitted (SRP-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AR017233; ASN04008.1; -  
 DR Complete proteome; Hypothetical protein.  
 KW SEQUENCE 227 AA; 24027 MW; 952EA4962C0BE199 CRC64;  
 SQ PT  
 Query Match 72.5%; Score 50; DB 2; Length 227;  
 Best Local Similarity 72.7%; Pred. No. 5.3; Mismatches 1; Indels 2; Gaps 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LKAMDPPTPLW 11  
 Db 146 LAALDPPTPLW 156

RESULT 7

ID ASN04008 PRELIMINARY; PRT; 227 AA.

AC ASN04008;  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DB Hypothetical protein.  
 KW MAP1691C.  
 OS Mycobacterium paratuberculosis.  
 OC Bacteria; Actinobacteria; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OC NCBI\_TaxID=1770;  
 RN RP  
 RC STRAIN=10;  
 RA Li L., Bannantine J., Zhang Q., Amongsin A., Alt D., Kapur V., Li L., Submitted (SRP-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AR017233; ASN04008.1; -  
 KW SEQUENCE 227 AA; 24027 MW; 952EA4962C0BE199 CRC64;  
 SQ PT  
 Query Match 72.5%; Score 50; DB 2; Length 227;  
 Best Local Similarity 72.7%; Pred. No. 5.3; Mismatches 1; Indels 2; Gaps 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LKAMDPPTPLW 11  
 Db 146 LAALDPPTPLW 156

RESULT 8

ID OTQB48 PRELIMINARY; PRT; 370 AA.

AC OTQB48;  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE AdCP7225 (Fragment)  
 GN Name=adCGG5196; ORFNames=ENSANGG0000014288;  
 OS Anopheles gambiae str. PEST.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
 OC NCBI\_TaxID=180454;  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=PEST;  
 RC Anophelidae Genome Sequencing Consortium;  
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RL -1- SIMILARITY: Contains 2 C2 domains.

RESULT 9

ID Q833V1 PRELIMINARY; PRT; 128 AA.

AC Q833V1;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DB Conserved domain protein.  
 DN Orderid=domainname=EF1825;  
 OS Enterococcus faecalis (streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OC NCBI\_TaxID=1351;  
 RN RP  
 RC STRAIN=10;  
 RA Sequence FROM N.A.  
 RL MIRN1=583 / ARCC 700802 /  
 SQ PT  
 Query Match 66.7%; Score 46; DB 2; Length 370;  
 Best Local Similarity 54.5%; Pred. No. 40; Mismatches 4; Indels 1; Gaps 0; Gaps 0;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LKAMDPPTPLW 11  
 Db 294 IRALDPPTPLW 304

RESULT 10

ID Q7QJ7 PRELIMINARY; PRT; 467 AA.

AC Q7QJ7;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 25, Last annotation update)  
 DE PRAM; PP00168; C2; PROSITE; PS50004; C2DOMAIN PROSITE; PS50004; C2\_DOMAIN\_2; 2.  
 DR PRINTS; PRO3360; C2DOMAIN PROSITE; PS50004; C2\_DOMAIN\_2; 2.  
 DR GO; GO:0005215; F:transporter activity; IEA.  
 DR GO; GO:005810; P:transport; IEA.  
 DR InterPro; IPR002149; Alatoxin\_recept.  
 DR InterPro; IPR00008; C2.  
 DR PRAM; PP00168; C2; PRINTS; PRO3360; C2DOMAIN PROSITE; PS50004; C2\_DOMAIN\_2; 2.  
 PT NON TER 1  
 SQ SEQUENCE 370 AA; 40989 MW; C558FDA3D5CD8D8P CRC64;  
 PT  
 Query Match 66.7%; Score 46; DB 2; Length 370;  
 Best Local Similarity 54.5%; Pred. No. 40; Mismatches 4; Indels 1; Gaps 0; Gaps 0;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LKAMDPPTPLW 11  
 Db ::::|:|||:|:  
 DR TIGR; EP1825; -  
 DR Complete proteome.  
 SQ SEQUENCE 128 AA; 14458 MW; 43459A9BE814572P CRC64;  
 SQ PT  
 Query Match 65.2%; Score 45; DB 2; Length 128;  
 Best Local Similarity 75.0%; Pred. No. 18; Mismatches 6; Indels 0; Gaps 0; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 DPPTPLW 12  
 Db 76 NPPTPLW 83

GN Name=oatv1;  
 OS Sub Scrofa; (Pig).  
 OC Eutheria; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suis; Suidae; Sub.  
 OX NCBI\_TaxID=9823;

[1] RN SEQUENCE FROM N.A.  
 RP TISSUE=Apical membrane of renal proximal tubule in kidney cortex;  
 RC MEDLINE=2255825; PubMed=1270363;  
 RA Jutabha P., Kanai Y., Hosoyamada M., Chairoungdua A., Kim D.K.,  
 RT Iribi Y., Babu E., Kim J.Y., Anzai N., Chatzidimitriou V., Endou H.,  
 RT "Identification of a novel voltage-driven organic anion transporter  
 present at apical membrane of renal proximal tubule.",  
 RL J. Biol. Chem. 278:27930-27938(2003).  
 DR EMBL; Ad04465; BAC0767611; -.  
 GO GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:005215; F: transporter activity; IEA.  
 DR GO; GO:0006810; P: transport; IEA.  
 DR InterPro; IPR007114; MPS.  
 PROSITE; PS50850; MFS; 1.  
 DR SQ SEQUENCE 467 AA; 52069 MW; 2B065005C3FDCA6 CRC64;

Query Match 65.2%; Score 45; DB 2; Length 467;  
 Best Local Similarity 58.3%; Pred. No. 74;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LKAMDPPTPPW 12  
 Db 255 IKAMIKSPPDWV 266

RESULT 11  
 Q8BXK6 PRELIMINARY; PRT; 242 AA.  
 ID Q8BXK6  
 AC OBXK6;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DB Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched  
 library, clone:B33018M03 product:hypothetical Fibronectin type III  
 DB structure containing protein, full insert sequence.  
 Name=B930041N14Rik;  
 OS Mus musculus (Mouse).  
 OC Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1] RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;  
 RA MEDLINE=99270253; PubMed=1039636;  
 RT Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.",  
 RL Math. Enzymol. 303:19-44(1999).  
 [2] RN SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Adrenal gland;  
 RC MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.",  
 RL Nature 409:685-690(2001).  
 RN [3] RP SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Adrenal gland;  
 RA "The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.",  
 RL Nature 420:563-573(2002).  
 [4] RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;  
 RA MEDLINE=20499374; PubMed=1102159;  
 RN Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RN Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",  
 RL Genome Res. 10:1617-1630(2000).  
 [5] RN SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Adrenal gland;  
 RC MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Ichijo M., Azawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Konno H., Akirema J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazzama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,  
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohra E., Watabiki M.,  
 RA Yoneeda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kura A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.",  
 RT Genome Res. 10:1757-1771(2000).  
 RN [6] RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;  
 RA Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Ichijo M., Kogawa T., Kasukawa T.,  
 RA Katoch H., Kawaji H., Kohlma Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurimura C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohbato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tateda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AK044537; BAC32775; 1; -.  
 DR MGD; MGI:244790; B930041N14Rik.  
 KW Hypothetical Protein.

SQ SEQUENCE 242 AA; 26120 MW; FD8FEE24EB934F8FO CRC64;

Query Match 63.8%; Score 44; DB 2; Length 242;  
 Best Local Similarity 77.8%; Pred. No. 53;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 AMDPPIPWL 11  
 Db 20 AVDPTEPGW 28

RESULT 12  
 Q18150 PRELIMINARY; PRT; 477 AA.  
 ID Q18150  
 AC Q18150;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Nuclear hormone receptor family protein 120.  
 GN Name=nr-120; ORFNames=c25BB.6;  
 OS Caenorhabditis elegans.  
 OC Bukay-Yota; Metazoa; Nemataoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Peloderaidae; Peloderae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1] RP SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RC MEDLINE=99069613; PubMed=9851916;  
 RA Wilson R.;  
 RT "Genome sequence of the nematode *C. elegans*: a platform for  
 RT investigating biology. The *C. elegans* Sequencing Consortium.",  
 RL Science 282:2012-2018(1998).  
 [2] RN SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Wilcox L.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.

RN [3] "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.  
 RP S9QUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Waterston R.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4] SEQUENCE FROM N.A.  
 RP STRAIN-Bristol N2;  
 RA Wilson R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.  
 RN [5] SEQUENCE FROM N.A.  
 RP STRAIN-Bristol N2;  
 RA Wilson R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
 CC -!- SIMILARITY: Belongs to the bacterial luciferase oxidoreductase family.  
 DR WormPEP; C05BB\_6; CB0877.  
 DR -!- SIMILARITY: Belongs to the nuclear hormone receptor family.  
 EMBL; U41356; ARK31912; -. DR HSSP; P20393; IACY.  
 DR GO; GO:005534; C:nucleus; IEA.  
 DR GO; GO:003700; P:transcription factor activity; IEA.  
 DR GO; GO:003655; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000336; Armon receptor lig.  
 DR InterPro; IPR005946; Str ncl receptor.  
 DR InterPro; IPR00324; VtD receptor.  
 DR InterPro; IPR0016288; Znf Costeroid.  
 DR Pfam; PF00104; Hormone recep; 1.  
 DR Pfam; PF0105; zf-C4; 1.  
 DR PRINTS; PR00047; STROIDPINGER.  
 DR SMART; SM0043; HOLI; 1.  
 DR SMART; SM0039; ZnF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
 DR DNA-binding; Metal-binding; Nuclear Protein; Receptor;  
 DR RNA-binding; Zinc finger.  
 KW TRANSCRIPTION  
 SQ SEQUENCE 477 AA; 54900 MW; 9D16ABPF3BBC0241 CRC64;

Query Match 63.8%; Score 44; DB 2; Length 477;  
 Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 KAMDPPTPIWI 12  
 Db 18 KLUHPSPPEWII 28

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RESULT 13

ID Y4VJ_RHISN	STANDARD;	PRT;	351 AA.
AC Q3218;			
DT 01-NOV-1997 (Rel. 35, Created)			
DT 01-JUL-2004 (Rel. 44, Last sequence update)			
DB Hypothetical protein Y4VJ.			
GN Rhizobium sp. (strain NGR234).			
OG Plasmid sym_PNGR234a.			
OC Bacteri; Protoprobacteria; Alphaproteobacteria; Rhizobiales;			
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.			
NCBI_TAXID=48291;			
[1]			
RP SEQUENCE FROM N.A.			
RC STRAIN-BR816;			
RA Luyten B., Verreth C., Vanderleyden J.,			
RL Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.			
[2] SEQUENCE FROM N.A.			
RC STRAIN-BR816;			
RA Luyten B., Swinnen B., Verreth C., Vlaesak K., Dombrecht B.,			
RA Vanderleyden J.,			
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.			
DR EMBL; U26451; ARAL1964; 1; .			
DR InterPro; IPR002103; Bac_luciferase.			
DR InterPro; IPR011251; Luciferase like.			
DR Pfam; PF00256; Bac_luciferase; 1.			
KW Plasmid.			
SQ SEQUENCE 354 AA; 39367 MW; 9D1B1A3F09BA70A42 CRC64;			

Query Match 62.3%; Score 43; DB 2; Length 354;  
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PTPLBLWI 12  
 Db 167 PTPIWI 173

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RESULT 15

Q846TB  
 ID Q846TB PRELIMINARY; PRT; 360 AA.  
 AC 0846TB;  
 DT 01-JUN-2003 (TREMBirel; 24, Created)  
 DT 01-JUN-2003 (TREMBirel; 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBirel; 25, Last annotation update)  
 DB Hypothetical adventurous gliding motility protein M.  
 GN Name=agmB;  
 OS Myxococcus xanthus.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;  
 OC Cystobacterineae; Myxococcaceae; Myxococcus.  
 OX NCBI\_TaxID=34;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hartzell, P.L.; Yonkerian, P.A.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.  
 CC -!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -!- SIMILARITY: Belongs to peptidase family M48.  
 DR EMBL; AY19758; AR066299.1;  
 DR GO; GO:0016020; Cimembrane; IEA.  
 DR GO; GO:004222; F-metalloendopeptidase activity; IEA.  
 DR GO; GO:006508; P-proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR01915; Peptidase M48.  
 DR PIR; P01435; Peptidase M48; 1.  
 KW Hydrolase; Hypothetical Protein; Metalloprotease; Protease; Zinc.  
 SEQUENCE 360 AA; 40304 MW; 98AB27E3EAEC023 CRC64;

Query Match 62.3%; Score 43; DB 2; Length 360;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 MDPTPPLWT 12  
 Db 332 MDPEPPRWV 340

Search completed: January 6, 2005, 10:17:48  
 Job time : 104.81 BECS

GenCore version 5.1.6  
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## Om protein - protein search, using sw model

Run on: January 6, 2005, 10:08:37 ; Search time 95.3513 Seconds  
(without alignment) 45.146 Million cell updates/sec.

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAMDPPPLWI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: geneseq\_23SeqP04:\*
- 2: geneseqP1990s:\*
- 3: geneseqP2000s:\*
- 4: geneseqP2001s:\*
- 5: geneseqP2002s:\*
- 6: geneseqP2003s:\*
- 7: geneseqP2003bs:\*
- 8: geneseqP2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID

Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	69	100.0	12	7	ABB80225	ABB80225	RESULT 1
2	69	100.0	15	2	AWM11575	ABB80225	standard; peptide; 12 AA.
3	69	100.0	15	2	AWM53841	XX	
4	69	100.0	15	7	ABB80223	XX	AC ABB80225;
5	65	94.2	11	7	ABB80226	XX	DT 06-NOV-2003 (first entry)
6	54	78.3	10	2	ABB80243	XX	DB Synthetic LTNF, LT-12.
7	54	78.3	10	7	ABB80222	XX	KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGF; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.
8	50	72.5	9	7	ABB80227	XX	KW OS Synthetic.
9	45	65.2	137	7	ADH88053	XX	KW PN WO2003060471-A2.
10	44	63.8	156	4	ABG28290	XX	PD 24-JUL-2003.
11	44	63.8	303	4	ABG18144	XX	PP 14-JAN-2003; 2003WO-US001044.
12	43	62.3	8	7	ABB80228	XX	PR 14-JAN-2002; 2002US-00047945.
13	43	62.3	393	4	AMT97984	XX	PT LIPPs BV, LIPPs FW;
14	43	62.3	932	8	ADM98800	XX	PT WPI; 2003-636703/60.
15	43	62.3	1189	2	ADM95496	XX	DR
16	43	62.3	1213	2	ADM06086	XX	PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.
17	43	62.3	1213	2	ADM25029	XX	PT Claim 7; Page 4; 24PP; English.
18	43	62.3	1219	4	ABB62618	XX	CC The sequences given in ABB80222-28 represent lethal toxin neutralising factor (LTNF) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid
19	42	60.9	94	4	AC02179	XX	CC
20	42	60.9	242	7	ADB90591	CC	CC
21	42	60.9	299	7	ADB90617	CC	CC
22	42	60.9	612	8	ADM39800	CC	CC
23	42	60.9	1336	6	ABR7496	CC	CC
24	42	60.9	1336	8	ADP18673	CC	CC
25	42	60.9	1457	4	AU032796	CC	CC

## ALIGNMENTS

26	41	59.4	9	6	ABR12621	Abri12621 Human can
27	41	59.4	9	6	ABR12017	Abri12017 Human can
28	41	59.4	9	6	ABR12854	Abri12854 Human can
29	41	59.4	10	6	ABR12743	Abri12743 Human can
30	41	59.4	10	6	ABR11875	Abri11875 Human can
31	41	59.4	10	6	ABR12121	Abri12121 Human can
32	41	59.4	10	6	ABR1298	Abri1298 Human can
33	41	59.4	10	6	ABR12106	Abri12106 Human can
34	41	59.4	10	6	ABR12294	Abri12294 Human can
35	41	59.4	10	6	ABR12738	Abri12738 Human can
36	41	59.4	15	6	ABR33125	Abri33125 Human can
37	41	59.4	15	6	ABR3388	Abri3388 Human can
38	41	59.4	15	6	ABR33116	Abri33116 Human can
39	41	59.4	15	6	ABR33427	Abri33427 Human can
40	41	59.4	15	6	ABR3353	Abri3353 Human can
41	41	59.4	37	4	ABR42105	Abi42105 Peptide #
42	41	59.4	37	4	AMW75798	Aam75798 Human bone
43	41	59.4	37	4	AMW2995	Aam62995 Human brain
44	41	59.4	37	4	ABD40295	Abi40295 Peptide #
45	41	59.4	64	4	AMW33978	Aam33978 Peptide #

Page  
2



DE N-terminus of opossum LTNF.  
 XX  
 KW LTNF; lethal toxin neutralising factor; opossum; envenomation; therapy;  
 KW anti-haemorrhagic protein; Elapidae; sea snake; Snake bite;  
 KW sepsis; allergy; bee sting; scorpion sting; plant toxin; bacterial toxin;  
 KW histamine reaction treatment.  
 XX OS Didelphis virginiana.  
 XX US5744449-A.  
 XX PD 28-APR-1998.  
 XX PP 03-JUN-1996; 96US-00657163.  
 XX PR 10-MAY-1993; 93US-00059387.  
 XX PR 22-SEP-1994; 94US-00310340.  
 XX PA (LIPPS/ LIPPS B V.  
 XX PA (LIPPS/ LIPPS F W.  
 XX PI LIPPS FW,  
 XX DR WPI; 1998-271108/24.  
 XX PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.  
 XX PS Claim 7; Col 11; 1LPP; English.  
 XX CC This sequence represents the peptide of the invention. It is a Lethal Toxin Neutralising Factor (LTNF) moiety from a 68 kDa anti-haemorrhagic protein derived from an opossum. The peptide can be used in a method for treating a victim of envenomation from a poisonous snake, preferably a poisonous snake from the family of Elapidae, Viperidae or Sea snake. It is useful for the treatment of snake bites, sepsis, allergies caused by the environment and treatment of bee or scorpion stings or toxicities caused by plant or bacterial toxins. The peptide can also be used in histamine reaction treatment. The peptide can be used in envenomation treatment for a variety of snakes without prior identification of the snake. Being short it can be synthetically prepared rather than the current production in horses, where some people can show hypersensitivity to horse proteins.  
 XX SQ Sequence 10 AA;

Query Match	78.3%	Score	54	DB	2	Length	10
Best Local Similarity	100.0%	Pred. No.	0.064				
Matches	10	Conservative	0	Mismatches	0	Indels	0
QY	1	1LKAMDPTPPL	10			Gaps	0
Db	1	1LKAMDPTPPL	10				

RESULT 7  
 ABB8022  
 ID ABB8022 standard; peptide; 10 AA.  
 AC ABB8022;  
 XX DT 06-NOV-2003 (first entry)  
 XX  
 XX DE Synthetic LTNF, LT-10.  
 XX  
 XX KW lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IGE; nerve growth factor; NCF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.  
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.  
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.  
 XX OS Synthetic.

XX PN WO2003060471-A2.  
 XX PD 24-JUL-2003.  
 XX PR 14-JAN-2003; 2003WO-US001044.  
 XX PR 14-JAN-2002; 2002US-00047945.  
 XX PA (LIPPS/ LIPPS B V.  
 XX PA (LIPPS/ LIPPS F W.  
 XX PI LIPPS BV, LIPPS FW;  
 XX DR WPI; 2003-636703/60.  
 XX PT Assaying a human endogenous protein (e.g. IgE, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.  
 XX PS Claim 7; Page 3; 24PP; English.  
 XX CC The sequences given in ABB8022-28 represent lethal toxin neutralising factor (LTNF) Peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin E (IgE), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgE levels, e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti-serum that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA.  
 XX SQ Sequence 10 AA;

Query Match	78.3%	Score	54	DB	7	Length	10
Best Local Similarity	100.0%	Pred. No.	0.064				
Matches	10	Conservative	0	Mismatches	0	Indels	0
QY	1	1LKAMDPTPPL	10			Gaps	0
Db	1	1LKAMDPTPPL	10				

RESULT 8  
 ABB8022  
 ID ABB8022 standard; peptide; 9 AA.  
 AC ABB8022;  
 XX DT 06-NOV-2003 (first entry)  
 XX DE Synthetic LTNF, LT-9.  
 XX KW Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin B; IGE; nerve growth factor; NCF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.  
 KW ADA; asthma; diabetes; autoimmune disease; systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.  
 KW Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.  
 XX OS Synthetic.

XX PN WO2003060471-A2.

PD	PA	(BUSH/) BUSH D.
XX	XX	Doucette-Stamm LA, Bush D;
PP	PI	
XX	XX	
PR	DR	WPI; 2003-95394-82.
XX	DR	N-PSDB; ADH84648.
PA	XX	New nucleic acid comprising a sequence encoding an <i>Enterococcus faecalis</i> polypeptide, useful for preparing a composition for diagnosing or treating B. <i>fecalis</i> infection.
XX	PT	
LIPPS BV,	PT	
XX	PT	
DR	XX	Disclosure; SEQ ID NO 5938; 193pp; English.
XX	PS	Claim 7; Page 4; 24pp; English.
PT	CC	The sequences given in ABC0222-28 represent lethal toxin neutralising factor (LTFN) peptides which may be used for reducing elevated levels of serum proteins selected from immunoglobulin G (IgG), nerve growth factor (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In particular, the methods of the invention are useful for diagnosing and treating conditions with elevated serum IgG levels e.g. asthma, diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease, Addison's disease or Hodgkin's disease) or depression. The efficacy of the protein may be monitored by assaying a human endogenous protein by performing an enzyme-linked immunosorbent assay (ELISA) on a saliva sample using an anti- <i>serum</i> that is specific for the protein. Saliva collection is relatively non-invasive when compared to blood collection for serum. Saliva can be centrifuged immediately, whereas blood requires clotting time before centrifugation to separate serum. Saliva proteins can be assayed by a simple ELISA test, whereas an assay of proteins from serum requires a more complicated sandwich type ELISA
XX	CC	Sequence 9 AA;
Query Match	CC	Best Local Similarity 72.5%; Score 50; DB 7; Length 9;
Matches	CC	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	CC	1 LKAMDPPTP 9
Db	CC	1 LKAMDPPTP 9
RESULT 9	CC	
ADH8053	ID	ABC22890 standard; protein; 137 AA.
XX	AC	ABC22890;
XX	XX	DT 18-FEB-2002 (first entry)
XX	DE	Novel human diagnostic protein #22891.
XX	KW	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; Homo sapiens.
XX	OS	
XX	PN	WO200175067-A2.
XX	XX	
DT	PD	11-OCT-2001.
XX	PP	30-MAR-2001; 2001WO-US008631.
XX	XX	
DE	PR	31-MAR-2000; 2000US-00540217.
XX	PR	23-AUG-2000; 2000US-00649167.
KW	XX	
KW	PA	(HYSB-) HYSBQ INC.
KW	XX	
KW	PT	Drmanac RT, Liu C, Tang YT;
KW	DR	WPI; 2001-639362/73.
XX	XX	
XX	DR	N-PSDB; AAS#7077.
PD	XX	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
XX	PT	
PR	XX	Claim 20; SEQ ID NO 53249; 103pp; English.
XX	PS	
PA	PS	

xx  
cc  
cc sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (III) and its binding partners are useful in medical imaging and to produce other types of data and products dependent on DNA and amino acid sequences. ABBG0010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

SQ Sequence 156 AA;

Query	Match	Score	DB	Length
Best	Local Similarity	63.8%	44	156
Matches	6; Conservative	54.5%	Pred. No.	38;
Qy	2 KAMDPPTPPLI 12		Mismatches	3;
Db	141 KAQPAPPWML 151		Indels	0;
			Gaps	0;

RESULT 11

ID	ABG18144	standard; protein; 303 AA.
ID	ABG18144	standard; protein; 303 AA.
AC	XX	
XX		
DT	18-FEB-2002	(first entry)
XX		
DE	Novel human diagnostic protein #18135.	
XX		
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.	
KW		
OS	Homo sapiens.	
XX		
PN	WO200175067-A2.	
XX		
PD	11-OCT-2001.	
XX		
PP	30-MAR-2001; 2001WO-US008631.	
XX		
PR	31-MAR-2000; 2000US-00540217.	
XX		
PA	(NYSE-) NYSEQ INC.	
XX		
PT	Dermatoc RT, Liu C, Tang YR;	
XX		
WPI	2001-639362/73.	
DR	N-FSDB; AAS82331.	
XX		

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. (III) and its binding partners are useful in medical imaging and to produce other types of data and products dependent on DNA and amino acid sequences. ABBG0010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

cc sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (III) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABBG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

SQ Sequence 303 AA;

Query	Match	Score	DB	Length
Best	Local Similarity	63.8%	44	303
Matches	6; Conservative	54.5%	Pred. No.	74;
Qy	2 KAMDPPTPPLI 12		Mismatches	3;
Db	39 BASDPVPPWY 49		Indels	0;
			Gaps	0;

RESULT 12

ID	ABB80228	standard; peptide; 8 AA.
ID	ABB80228	standard; peptide; 8 AA.
AC	XX	
XX		
DT	06-NOV-2003	(first entry)
XX		
DE	Synthetic LTNF, LT-8.	
XX		
KW	Lethal toxin neutralising factor; LTNF; serum protein; immunoglobulin E; IGB; nerve growth factor; NGF; insulin; myoglobin; adenosine deaminase; ADA; asthma; diabetes; autoimmune disease; Systemic lupus erythematosus; SLE; rheumatoid arthritis; Sjogren's syndrome; Reiter's syndrome; Graves' disease; Addison's disease; Hodgkin's disease; depression; saliva; ELISA.	
KW		
OS	Synthetic.	
XX		
PN	WO2003060471-A2.	
XX		
PD	24-JUL-2003.	
XX		
PR	14-JAN-2003; 2003WO-US001044.	
XX		
PR	14-JAN-2002; 2002US-00047945.	
XX		
PA	(LIPP/) LIPPS B V.	
PA	(LIPP/) LIPPS F W.	
XX		
PT	Lipps BV, Lipps FW;	
XX		
DR	WPI; 2003-636703/60.	
XX		
PT	Assaying a human endogenous protein (e.g. IGB, nerve growth factor, insulin or adenosine deaminase or myoglobin), useful for diagnosing e.g. asthma or diabetes, by employing an ELISA on a saliva sample from a patient.	
PT		
PS	Claim 7; Page 4; 24pp; English.	
XX		
PS		

CC The sequences given in ABB00222-28 represent lethal toxin neutralising  
 CC factor (LTFN) peptides which may be used for reducing elevated levels of  
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor  
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In  
 CC particular, the methods of the invention are useful for diagnosing and  
 CC treating conditions with elevated serum IgE levels, e.g. asthma,  
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid  
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,  
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of  
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva  
 CC sample using an anti-serum that is specific for the protein. Saliva  
 CC collection is relatively non-invasive when compared to blood collection  
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires  
 CC clotting time before centrifugation to separate serum. Saliva proteins  
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from  
 CC serum requires a more complicated sandwich type ELISA.

SQ Sequence 8 AA;

Query	Match	Score	DB	Length
Best	Local Similarity	62.3%	7	8
Matches	8;	Pred. No.	1.7e+06	
Oy	1 LKAMDPTP	0		
Db	1 LKAMDPTP	8		

RESULT 13

AAW79784 standard; protein; 393 AA.

AC AAM79784;

DT 06-NOV-2001 (first entry)

DB Human protein SEQ ID NO 3430.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;  
 KW tissue growth factor; immunomodulator; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation.  
 OS Homo sapiens.  
 XX W0200157190-A2.

PD 09-AUG-2001.

PP 05-FEB-2001; 2001WO-US004098.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-0059805.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663551.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

PA (HYSE-) HYSEQ INC.

PT Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Weijman T, Goodrich R;

XX WPI; 2001-476283/51.

DR N-PSDB; AAK52917.

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful  
 PT in diagnosis and gene therapy.

XX

CC The sequences given in ABB00222-28 represent lethal toxin neutralising  
 CC factor (LTFN) peptides which may be used for reducing elevated levels of  
 CC serum proteins selected from immunoglobulin E (IgE), nerve growth factor  
 CC (NGF), insulin, myoglobin and/or adenosine deaminase (ADA). In  
 CC particular, the methods of the invention are useful for diagnosing and  
 CC treating conditions with elevated serum IgE levels, e.g. asthma,  
 CC diabetes, autoimmune disease (e.g. erythematosus (SLE), rheumatoid  
 CC arthritis, Sjogren's syndrome, Reiter's syndrome, Graves' disease,  
 CC Addison's disease or Hodgkin's disease) or depression. The efficacy of  
 CC performing an enzyme-linked immunosorbent assay (ELISA) on a saliva  
 CC sample using an anti-serum that is specific for the protein. Saliva  
 CC collection is relatively non-invasive when compared to blood collection  
 CC for serum. Saliva can be centrifuged immediately, whereas blood requires  
 CC clotting time before centrifugation to separate serum. Saliva proteins  
 CC can be assayed by a simple ELISA test, whereas an assay of proteins from  
 CC serum requires a more complicated sandwich type ELISA.

PS Claim 20; Page 332; 6221pp; English.  
 XX

CC The invention relates to poly nucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAW8323-AAM80302) that exhibit activity eliciting to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC poly nucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibit activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
 CC (AAK52582) and 3666 (AAM8020) are omitted as the relevant pages from the  
 CC sequence listing were missing at the time of publication

SQ Sequence 393 AA;

Query	Match	Score	DB	Length
Best	Local Similarity	62.3%	4	393
Matches	6;	Pred. No.	1.4e+02	
Oy	1 LKAMDPRLW	11		
Db	11 IKLUSPLPPLW	21		

RESULT 14

ID AAM98800  
 ID AAM98800 standard; protein; 932 AA.

AC ADM98800;

DT 01-JUL-2004 (first entry)

DB HMG-CoA reductase polypeptide #53.

KW Geranylgeranyl pyrophosphate synthase; diterpene; diterpene precursor;  
 KW diterpene synthase; defence toxin; volatile defensive signal;  
 KW pollinator attractant; photoprotectant; HMG-CoA reductase; enzyme.

OS Strongylocentrotus purpuratus.

XX US2004072323-A1.

PN

PD 15-APR-2004.

XX PP 07-JAN-2002; 2002US-00041018.

XX PR 05-JAN-2001; 2001US-0259800P.

XX PA (MATS-) MATSUDA S P T.

PA (HART-) HART B A.

XX PI Matsuda SPT, Hart BA;

XX DR WPI; 2004-373921/35.

PT New unicellular organisms comprising exogenous nucleic acids encoding a  
 PT geranylgeranyl pyrophosphate and a diterpene synthase, useful for  
 PT producing diterpenes and diterpene precursors.

XX Disclosure; SEQ ID NO 220; 38pp; English.

CC The invention relates to a unicellular organism for producing a diterpene  
 CC or diterpene precursor comprising an exogenous nucleic acid sequence  
 CC encoding a geranylgeranyl pyrophosphate synthase under the control of a  
 CC promoter operable in the organism, and an exogenous nucleic acid sequence  
 CC encoding a diterpene synthase under the control of a promoter operable in  
 CC the organism. The invention also relates to methods of producing a  
 CC diterpene or diterpene precursor and a method of isolating a diterpene  
 CC synthesis comprising growing several cells in the presence of a  
 CC polyaromatic resin to make a cell/resin mixture, where at least one of

CC the cells further comprises at least one isolated and purified nucleic  
 CC acid sequence of a yeast expression library, and the expression of the  
 CC nucleic acid sequence is regulated by an inducible promoter under  
 CC conditions where the expression is induced, filtering the cell/resin  
 mixture, extracting the cell/resin mixture with alcohol to produce an  
 CC organic eluent and analysing the organic eluent by a screening method  
 CC including chromatography and/or spectroscopy, to identify the nucleic  
 acid sequence encoding the diterpene synthase. The unicellular  
 CC microorganism is useful as a diterpene or diterpene precursor producing  
 CC system. Diterpenes, in plants, serve as defence toxins, volatile  
 CC defensive signals, pollinator attractants and photoprotectants. This  
 CC sequence represents an HMG-CoA reductase polypeptide used in the scope of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification but was obtained in electronic format from  
 CC USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 932 AA;

Query Match 62.3%; Score 43; DB 8; Length 932;  
 Best Local Similarity 70.0%; Pred. No. 3.3e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KAMDPPIPW 11  
 Db 298 KKIDPTMPMLW 307

RESULT 15

AAR56496  
 ID AAR56496 standard; protein; 1189 AA.  
 AC  
 XX  
 AC AAR56496;  
 XX  
 AC  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 23-MAR-1995 (first entry)  
 DE TATA-binding protein-associated factor dTAF150.  
 XX  
 KW TATA-binding protein associated factor; dTAF150; screening; diagnostic;  
 KW therapeutic; gene transcription regulation.  
 OS Drosophila.  
 XX  
 Key Location/Qualifiers  
 FH  
 FT Misc-difference 923  
 PT /note= "Val or Leu"  
 FT Misc-difference 1106  
 PT /note= "Arg, Pro or His"  
 PT Misc-difference 1172  
 PT /note= "STOP"  
 PT Misc-difference 1176  
 PT /note= "STOP"  
 XX  
 PN WO9417087-A1.  
 XX  
 PD 04-AUG-1994.  
 XX  
 PP 28-JAN-1994; 94WO-US001114.  
 XX  
 PR 28-JAN-1993; 93US-00013412.  
 PR 30-JUN-1993; 93US-00087119.  
 XX  
 PA (RBGC ) UNIV CALIFORNIA.  
 XX  
 PI Tjian R, Comai L, Dynlacht BD, Hoey T, Ruppert S, Tanese N;  
 PI Wang E, Weinzierl ROJ;  
 XX  
 DR WPI; 1994-264019/32.  
 XX  
 N-PSDB; AQ070733.

TATA-binding protein associated protein factors - and corresponding  
 PT nucleotide sequence and deriv. antibodies, useful in screening,  
 PT diagnostics and therapeutics.

XX Disclosure: Page 156; 180pp; English.

XX  
 PS The TATA-binding protein associated factor dTAF150 (including specific  
 CC antibodies and fusion products) are used in drug screening, diagnostics  
 CC and therapeutics. They are used in the development of specific  
 CC biochemical assays for screening compounds that agonise or antagonise  
 CC selected transcription factors involved in regulating gene expression  
 CC associated with human pathology. (updated on 25-MAR-2003 to correct PN  
 CC field.)

XX Sequence 1189 AA;

Query Match 62.3%; Score 43; DB 2; Length 1189;  
 Best Local Similarity 66.7%; Pred. No. 4.2e+02;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKAMDPPIWL 12  
 Db 589 LSAMDSPVLI 600

Search completed: January 6, 2005, 10:22:48  
 Job time : 96.3513 secs

Gencore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 6, 2005, 10:23:04 ; Search time 81.0811 seconds  
(without alignments)  
53.365 Million cell updates/sec

Title: US-10-047-945-4

Perfect score: 69

Sequence: 1 LKAMDPTPPLWI 12

Scoring table: BLOSUM62  
Gapext 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /cgm2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep: \*  
4: /cgm2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep: \*  
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20: /cgm2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	69	100.0	12	14	US-10-047-945-4
2	69	100.0	15	14	US-10-047-945-2
3	65	94.2	11	14	US-10-047-945-5
4	54	78.3	10	14	US-10-047-945-4
5	50	72.5	9	14	US-10-047-945-6
6	44	63.8	106	15	US-10-042-2550201
7	44	63.8	124	15	US-10-042-15167
8	44	63.8	144	15	US-10-042-599-205702
9	43	62.3	8	14	US-10-047-945-7
10	43	62.3	115	17	US-10-425-115-322493
11	43	62.3	129	16	US-10-431-963-168841
12	43	62.3	932	15	US-10-041-018-220
13	42	60.9	82	16	US-10-437-963-128480

RESULT 1  
US-10-047-945-4  
; Sequence 4, Application US/10047945

; Publication No. US2003015755A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPPS, FREDERICK W.  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT FOR IMMUNOGLOBULIN B  
; TITLE OF INVENTION: (1QB) IMPLICATED DISORDERS  
; FILE REFERENCE: FWPAT015US  
; CURRENT APPLICATION NUMBER: US/10/047-945  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-12 of 2 above.

US-10-047-945-4  
Query Match 100%; Score 69; DB 14; Length 12;  
Best Local Similarity 100%; Pred. No. 0.001%; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 0; MisMatches 0; Indels 0; Gaps 0;  
Qy 1 LKAMDPTPPLWI 12  
Db 1 LKAMDPTPPLWI 12  
RESULT 2



RESULT 8 ; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 205702 ; LENGTH: 144  
; LENGTH: 144 ;  
; TYPE: PRT ;  
; ORGANISM: Glycine max ;  
; FEATURE: NAME/KEY: unsure ;  
; LOCATION: (1)..(144) ;  
; OTHER INFORMATION: unsure at all Xaa locations ;  
; FEATURE: OTHER INFORMATION: Clone ID: PAT\_MRT3847\_2777C.1.pep ;  
; SEQ ID NO 255201 ;  
; LENGTH: 106 ;  
; TYPE: PRT ;  
; ORGANISM: Glycine max ;  
; FEATURE: OTHER INFORMATION: Score 44; DB 15; Length 106; ;  
; OTHER INFORMATION: Best Local Similarity 85.7%; Pred. No. 48; ;  
; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; ;  
; US-10-424-599-255201 ;  
; Query Match ;  
; Best Local Similarity 63.8%; Score 44; DB 15; Length 106; ;  
; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0; ;  
; Qy 6 PTPPLWI 12 ;  
; Db 92 PTPPLWV 98 ;  
; RESULT 7 ;  
; Sequence 151167 ;  
; Publication No. US20040031072A1 ;  
; GENERAL INFORMATION: ;  
; APPLICANT: La Rosa, Thomas J ;  
; APPLICANT: Kovalic, David K ;  
; APPLICANT: Zhou, Yihua ;  
; APPLICANT: Cao, Yongwei ;  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement ;  
; FILE REFERENCE: 38-21(53223)B ;  
; CURRENT FILING DATE: 2003-04-28 ;  
; NUMBER OF SEQ ID NOS: 285684 ;  
; SEQ ID NO 151167 ;  
; LENGTH: 124 ;  
; TYPE: PRT ;  
; ORGANISM: Glycine max ;  
; FEATURE: OTHER INFORMATION: Clone ID: PAT\_MRT3847\_107527C.1.pep ;  
; US-10-424-599-151167 ;  
; Query Match ;  
; Best Local Similarity 63.8%; Score 44; DB 15; Length 124; ;  
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0; ;  
; Qy 5 DPTPPLWI 12 ;  
; Db 96 DPTPPLWV 103 ;  
; RESULT 8 ;  
; Sequence 205702, Application US/10424599 ;  
; Publication No. US20040031072A1 ;  
; GENERAL INFORMATION: ;  
; APPLICANT: La Rosa, Thomas J ;  
; APPLICANT: Kovalic, David K ;  
; APPLICANT: Zhou, Yihua ;  
; APPLICANT: Cao, Yongwei ;  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement ;  
; FILE REFERENCE: 38-21(53223)B ;  
; CURRENT FILING DATE: 2003-04-28 ;  
; NUMBER OF SEQ ID NOS: 285684 ;  
; SEQ ID NO 151167 ;  
; LENGTH: 124 ;  
; TYPE: PRT ;  
; ORGANISM: Glycine max ;  
; FEATURE: OTHER INFORMATION: Score 44; DB 15; Length 124; ;  
; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0; ;  
; Qy 5 DPTPPLWI 12 ;  
; Db 96 DPTPPLWV 103 ;  
; RESULT 9 ;  
; Sequence 151167 ;  
; Publication No. US20030157552A1 ;  
; GENERAL INFORMATION: ;  
; APPLICANT: LIPPS, BINIE V. ;  
; APPLICANT: LIPPS, FREDERICK W. ;  
; TITLE OF INVENTION: DIAGNOSTIC AND TREATMENT FOR IMMUNOGLOBULIN B DISORDERS ;  
; FILE REFERENCE: FWPAT015US ;  
; CURRENT APPLICATION NUMBER: US/10/047,945 ;  
; CURRENT FILING DATE: 2002-01-14 ;  
; PRIOR APPLICATION NUMBER: ;  
; PRIOR FILING DATE: ;  
; NUMBER OF SEQ ID NOS: 7 ;  
; SEQ ID NO 7 ;  
; LENGTH: 8 ;  
; TYPE: PRT ;  
; SOFTWARE: WORDPERFECT 5.1 FOR WINDOWS ;  
; FEATURE: NAME/KEY: ;  
; OTHER INFORMATION: OTHER INFORMATION: Artificial Sequence ;  
; ORGANISM: Artificial Sequence ;  
; LOCATION: ;  
; OTHER INFORMATION: Synthetic. Corresponds to fragment 1-8 of 2 above. ;  
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; Query Match ;  
; Best Local Similarity 62.3%; Score 43; DB 14; Length 8; ;  
; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ;  
; Qy 1 LKAMDPITP 8 ;  
; Db 1 LKAMDPITP 8 ;  
; RESULT 10 ;  
; Sequence 322493, Application US/10425115 ;  
; Publication No. US20040214272A1 ;  
; GENERAL INFORMATION: ;  
; APPLICANT: La Rosa, Thomas J. ;  
; APPLICANT: Kovalic, David K. ;  
; APPLICANT: Zhou, Yihua ;  
; APPLICANT: Cao, Yongwei ;  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants ;  
; FILE REFERENCE: 38-21(53223)B ;  
; CURRENT APPLICATION NUMBER: US/10/425,115 ;  
; CURRENT FILING DATE: 2003-04-28 ;  
; NUMBER OF SEQ ID NOS: 369325 ;  
; SEQ ID NO 322493 ;

RESULT 11  
US-10-437-963-168841  
Query Match 62.3%; Score 43; DB 17; Length 115;  
Best Local Similarity 75.0%; Pred. No. 72; Mismatches 1; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPPLWI 12  
Db 43 DPTPENWV 50

RESULT 11  
US-10-437-963-168841  
Sequence 158841, Application US/10437963  
Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 168841 LENGTH: 129

TYPE: PRT ORGANISM: Oryza sativa

FEATURE: OTHER INFORMATION: Clone ID: PAT\_MRT4530\_67316C.1.pep

RESULT 12  
US-10-041-018-220  
Query Match 62.3%; Score 43; DB 16; Length 129;  
Best Local Similarity 63.6%; Pred. No. 81; Mismatches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LKAMDPTPPNW 11  
Db 84 LARMPPSPPLW 94

RESULT 12  
US-10-041-018-220  
Sequence 220, Application US/10441018  
Publication No. US2004007223A1

GENERAL INFORMATION:

APPLICANT: Matsuda, Seiichi P.T.

APPLICANT: Hart, Elizabeth A.

TITLE OF INVENTION: Diterpene-producing Unicellular Organism FILE REFERENCE: P02000US11002547 CURRENT APPLICATION NUMBER: US/10/041,018 CURRENT FILING DATE: 2003-01-07 PRIORITY APPLICATION NUMBER: US 60/259880 PRIORITY FILING DATE: 2001-01-05 NUMBER OF SEQ ID NOS: 413 SOFTWARE: PatentIn version 3.1 SEQ ID NO 220 LENGTH: 932

TYPE: PRT ORGANISM: Strongylocentrotus purpuratus

RESULT 13  
US-10-437-963-128480  
Query Match 62.3%; Score 43; DB 15; Length 932;  
Best Local Similarity 70.0%; Pred. No. 5.1e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAMDPPLW 11  
Db 298 KKIDPTIMPLW 307

RESULT 13  
US-10-437-963-128480  
Sequence 128480, Application US/10437963  
Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 128480 LENGTH: 82

TYPE: PRT ORGANISM: Oryza sativa

FEATURE: OTHER INFORMATION: Clone ID: PAT\_MRT4530\_30829C.1.pep

RESULT 14  
US-10-177-293-228  
Query Match 60.9%; Score 42; DB 16; Length 82;  
Best Local Similarity 75.0%; Pred. No. 75; Mismatches 6; Conservative 1; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DPTPPLWI 12  
Db 75 BPTPPCWLI 82

RESULT 14  
US-10-177-293-228  
Sequence 228, Application US/10177293  
Publication No. US20030124128A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Glatt, Karen

APPLICANT: Zhao, Xumei

APPLICANT: Gammavarpu, Manjula

APPLICANT: Kamatkar, Shubhangi

APPLICANT: Mertens, Maureen

APPLICANT: Meyer, Vic

APPLICANT: Wang, Youzhen

APPLICANT: Xu, Yongyao

APPLICANT: Hoerisch, Sebastian

APPLICANT: Mahan, John

APPLICANT: Meyers, Rachel E.

APPLICANT: Bast Jr., Robert C.

APPLICANT: Horrobagyi, Gabriel N.

APPLICANT: Puszta, Lajos

APPLICANT: Metc, Funda

APPLICANT: Sahin, Aysegul

APPLICANT: Mill, Gordon B.

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, FILE REFERENCE: MRI-031 CURRENT APPLICATION NUMBER: US/10/177,293 CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US 60/299, 887  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: US 60/301, 572  
PRIOR FILING DATE: 2001-06-27  
PRIOR APPLICATION NUMBER: US 60/306, 501  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: US 60/325, 002  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: US 60/362, 585  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/xxx, xxx  
PRIOR FILING DATE: 2002-05-14  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 228  
LENGTH: 1336  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-177-293-228

RESULT 15  
US-09-864-761-45321  
Sequence 45321, Application US/09864761  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Ascomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864, 761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180, 312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207, 456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632, 366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263, 6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236, 359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30

Query Match 60.9%; Score 42; DB 14; Length 1336;  
Best Local Similarity 77.8%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Other Information: EXPRESSED IN BONE MARROW, SIGNAL = 0.68

Qy 4 MDPTPPMLI 12  
Db 34 MDPQPBLWT 42

RESULT 15  
US-09-864-761-45321  
Sequence 45321, Application US/09864761  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Ascomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864, 761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180, 312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207, 456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632, 366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263, 6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236, 359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30

Query Match 59.4%; Score 41; DB 9; Length 37;  
Best Local Similarity 54.5%; Pred. No. 50; Mismatches 6; Conservative 2; Other Information: EXPRESSED IN BRAIN, SIGNAL = 0.68  
Matches 6; Other Information: SWISSPROT HIT: A198481.1, EVALUE 6.40e+00  
Indels 3; Gaps 0; Other Information: EST-HUMAN HIT: A198481.1, EVALUE 6.00e-16  
Db 5 KSMGPAPPWM 15

Search completed: January 6, 2005, 10:44:44  
Job time : 82.081 secs

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## ON protein - protein search, using SW model

Run on: January 6, 2005, 10:09:51 ; Search time 24.3243 Seconds  
(without alignments)  
32.717 Million cell updates/sec

Title: US-10-047-945-4  
Perfect score: 69  
Sequence: 1 LKAMDPTPPLWI 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgmn\_2\_6/ptodata/1/iaa/5A\_COMB.pep: \*  
2: /cgmn\_2\_6/ptodata/1/iaa/5B\_COMB.pep: \*  
3: /cgmn\_2\_6/ptodata/1/iaa/6A\_COMB.pep: \*  
4: /cgmn\_2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
5: /cgmn\_2\_6/ptodata/1/iaa/PCTUS\_COMB.pep: \*  
6: /cgmn\_2\_6/ptodata/1/iaa/backFiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	69	100.0	15 1	US-08-310-3401-1 Sequence 1, Appl 1 Sequence 1, Appl 1 Sequence 2, Appl 1 Sequence 5338, Ap
2	69	100.0	15 1	US-08-310-3401-1 Sequence 1, Appl 1 Sequence 2, Appl 1 Sequence 5338, Ap
3	54	78.3	10 1	US-08-657-1634-2 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 492, Ap
4	45	65.2	137 4	US-08-134-000-5938 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 492, Ap
5	43	62.3	1213 1	US-08-188-582-20 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 492, Ap
6	43	62.3	1213 1	US-08-646-15-20 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 492, Ap
7	41	59.4	212 4	US-10-140-002-482 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 492, Ap
8	41	59.4	253 4	US-09-270-767-4323 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 492, Ap
9	40	58.0	198 4	US-09-270-767-57545 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 492, Ap
10	40	58.0	360 4	US-09-270-767-42265 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 20, Appl 1 Sequence 492, Ap
11	39	56.5	205 2	US-08-477-3961-18 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 492, Ap
12	39	56.5	210 4	US-09-270-67-45215 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 492, Ap
13	38	55.1	267 2	US-07-857-2248-42 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 492, Ap
14	38	55.1	1740 4	US-09-377-248-40 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 492, Ap
15	37	53.6	15 3	US-08-603-998-444 Sequence 44, Appl 1 Sequence 44, Appl 1 Sequence 44, Appl 1 Sequence 44, Appl 1
16	37	53.6	15 4	US-09-500-124-444 Sequence 44, Appl 1 Sequence 44, Appl 1 Sequence 44, Appl 1 Sequence 44, Appl 1
17	37	53.6	78 4	US-09-248-796-21988 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 4521, Ap
18	37	53.6	87 4	US-09-270-67-41296 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 4521, Ap
19	37	53.6	87 4	US-09-270-67-56512 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 4521, Ap
20	37	53.6	196 4	US-09-252-910-26983 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1 Sequence 18, Appl 1
21	37	53.6	207 4	US-09-328-352-6054 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1
22	37	53.6	210 4	US-09-071-035-232 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1
23	37	53.6	256 4	US-09-071-035-230 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1
24	37	53.6	265 4	US-09-270-67-43480 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1
25	37	53.6	291 4	US-09-134-000-66676 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1
26	37	53.6	306 4	US-09-124-000-6583 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1 Sequence 22, Appl 1
27	37	53.6	387 4	US-09-252-991A-30473 Sequence 30473, Ap

## ALIGNMENTS

28	37	53.6	427 4	US-08-311-731A-216 Sequence 216, App
29	37	53.6	502 4	US-09-540-236-3413 Sequence 3413, App
30	37	53.6	528 4	US-09-270-767-42895 Sequence 42895, App
31	37	53.6	3170 3	US-07-442-734C-5 Sequence 5, App
32	37	53.6	3170 3	US-08-339-009A-5 Sequence 5, App
33	37	53.6	4928 3	US-09-036-987A-5 Sequence 7, App
34	37	53.6	4928 3	US-09-310-700-5 Sequence 7, App
35	37	53.6	4928 4	US-09-603-207-5 Sequence 178, App
36	36	52.2	119 4	US-09-248-796A-25521 Sequence 13655, App
37	36	52.2	200 4	US-09-232-991A-27890 Sequence 13655, App
38	36	52.2	230 3	US-09-787-739-7 Sequence 15934, App
39	36	52.2	230 4	US-09-989-903-7 Sequence 20624, App
40	36	52.2	280 3	US-09-247-155-178 Sequence 45869, App
41	36	52.2	323 4	US-09-489-039A-13655 Sequence 42848, App
42	36	52.2	338 4	US-09-248-796A-15934 Sequence 42848, App
43	36	52.2	338 4	US-09-248-796A-20624 Sequence 42848, App
44	36	52.2	409 4	US-09-210-767-42848 Sequence 42848, App
45	36	52.2	498 4	US-09-210-767-42848 Sequence 42848, App

INDIVIDUAL ISOLATE: TEXAS WILD  
 DEVELOPMENTAL STAGE: ADULT  
 HAPLOTYPE:  
 TISSUE TYPE: BLOOD  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE: OPOSSUM SERA SEQ ID NO: 1:  
 LIBRARY:  
 CLONE:

PUBLICATION INFORMATION:  
 AUTHORS: JONAS PERALES, ET AL.  
 TITLE: ANTI-SNAKE VENOM FORM DIDELPHIDAE  
 JOURNAL: INTERNATIONAL SOCIETY ON  
 TOXICOLOGY  
 VOLUME: 10TH WORLD CONGRESS ON ANIMAL  
 VOLUME: PLANT AND MICROBIAL TOXINS 3-8 NOV 1991,  
 ISSUE: PROGRAMME AND ABSTRACTS  
 PAGES: 104  
 DATE: 3-8 NOV 1991  
 US-08-310-340A-1

Query Match 100.0%; Score 69; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPWI 12  
 Db 1 LKAMDPPTPWI 12

RESULT 2

US-08-657-163A-1

; Sequence 1, Application US/08657163A

; Patent No. 574449

GENERAL INFORMATION:  
 APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
 SYNTHETIC LTNFS AND THEIR  
 TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.

CITY: BELLAIRE

STATE: TEXAS

COUNTRY: USA

ZIP: 77401

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,163A

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/310,340

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

APPLICATION NUMBER: 08/058,387

FILING DATE: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME: JOHN R. CASPERSON

REGISTRATION NUMBER: 28,198

REFERENCE DOCKET NUMBER: FWL-PAT-US-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-482-2961

TELEFAX: 713-663-7290

TELEX:

INFORMATION FOR SEQ ID NO: 1:

Query Match 100.0%; Score 69; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPWI 12  
 Db 1 LKAMDPPTPWI 12

RESULT 2

US-08-657-163A-1

; Sequence 1, Application US/08657163A

; Patent No. 574449

GENERAL INFORMATION:  
 APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
 SYNTHETIC LTNFS AND THEIR  
 TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.

CITY: BELLAIRE

STATE: TEXAS

COUNTRY: USA

ZIP: 77401

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,163A

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/310,340

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

APPLICATION NUMBER: 08/058,387

FILING DATE: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME: JOHN R. CASPERSON

REGISTRATION NUMBER: 28,198

REFERENCE DOCKET NUMBER: FWL-PAT-US-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-482-2961

TELEFAX: 713-663-7290

TELEX:

INFORMATION FOR SEQ ID NO: 1:

Query Match 100.0%; Score 69; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPWI 12  
 Db 1 LKAMDPPTPWI 12

RESULT 3

US-08-657-163A-2

; Sequence 2, Application US/08657163A

; Patent No. 574449

GENERAL INFORMATION:  
 APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
 SYNTHETIC LTNFS AND THEIR  
 TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.

CITY: BELLAIRE

STATE: TEXAS

COUNTRY: USA

ZIP: 77401

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,163A

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/310,340

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

APPLICATION NUMBER: 08/058,387

FILING DATE: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME: JOHN R. CASPERSON

REGISTRATION NUMBER: 28,198

REFERENCE DOCKET NUMBER: FWL-PAT-US-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-482-2961

TELEFAX: 713-663-7290

TELEX:

INFORMATION FOR SEQ ID NO: 1:

Query Match 100.0%; Score 69; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPWI 12  
 Db 1 LKAMDPPTPWI 12

RESULT 3

US-08-657-163A-2

; Sequence 2, Application US/08657163A

; Patent No. 574449

GENERAL INFORMATION:  
 APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
 SYNTHETIC LTNFS AND THEIR  
 TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.

CITY: BELLAIRE

STATE: TEXAS

COUNTRY: USA

ZIP: 77401

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,163A

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/310,340

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

APPLICATION NUMBER: 08/058,387

FILING DATE: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME: JOHN R. CASPERSON

REGISTRATION NUMBER: 28,198

REFERENCE DOCKET NUMBER: FWL-PAT-US-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-482-2961

TELEFAX: 713-663-7290

TELEX:

INFORMATION FOR SEQ ID NO: 1:

Query Match 100.0%; Score 69; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPWI 12  
 Db 1 LKAMDPPTPWI 12

RESULT 3

US-08-657-163A-2

; Sequence 2, Application US/08657163A

; Patent No. 574449

GENERAL INFORMATION:  
 APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
 SYNTHETIC LTNFS AND THEIR  
 TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.

CITY: BELLAIRE

STATE: TEXAS

COUNTRY: USA

ZIP: 77401

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,163A

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/310,340

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

APPLICATION NUMBER: 08/058,387

FILING DATE: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME: JOHN R. CASPERSON

REGISTRATION NUMBER: 28,198

REFERENCE DOCKET NUMBER: FWL-PAT-US-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-482-2961

TELEFAX: 713-663-7290

TELEX:

INFORMATION FOR SEQ ID NO: 1:

Query Match 100.0%; Score 69; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPWI 12  
 Db 1 LKAMDPPTPWI 12

RESULT 3

US-08-657-163A-2

; Sequence 2, Application US/08657163A

; Patent No. 574449

GENERAL INFORMATION:  
 APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
 SYNTHETIC LTNFS AND THEIR  
 TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.

CITY: BELLAIRE

STATE: TEXAS

COUNTRY: USA

ZIP: 77401

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" FLOPPY DISK, 1.44 MB

COMPUTER: IBM COMPATIBLE  
 OPERATING SYSTEM: MS-DOS 5.0/WINDOWS 3.1  
 SOFTWARE: MS WORD 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,163A

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/310,340

FILING DATE: 22 SEPTEMBER 1994

CLASSIFICATION: 514

APPLICATION NUMBER: 08/058,387

FILING DATE: 10 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME: JOHN R. CASPERSON

REGISTRATION NUMBER: 28,198

REFERENCE DOCKET NUMBER: FWL-PAT-US-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-482-2961

TELEFAX: 713-663-7290

TELEX:

INFORMATION FOR SEQ ID NO: 1:

Query Match 100.0%; Score 69; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKAMDPPTPWI 12  
 Db 1 LKAMDPPTPWI 12

RESULT 3

US-08-657-163A-2

; Sequence 2, Application US/08657163A

; Patent No. 574449

GENERAL INFORMATION:  
 APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS  
 TITLE OF INVENTION: EMBODIMENTS OF NATURAL AND  
 SYNTHETIC LTNFS AND THEIR  
 TITLE OF INVENTION: UTILITY AS TREATMENT FOR ENVENOMATION  
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: BINIE V. LIPPS  
 STREET: 4509 MIMOSA DR.

CITY: BELLAIRE

STATE: TEXAS

COUNTRY: USA

ZIP: 77401

COMPUTER READABLE FORM:

&lt;p

APPLICATION NUMBER: 08/058,387 ;  
 FILING DATE: 10 MAY 1993 ;  
 ATTORNEY/AGENT INFORMATION: ;  
 NAME: JOHN R. CASPERSON ;  
 REGISTRATION NUMBER: 28,198 ;  
 REFERENCE/DOCKET NUMBER: FMT-PAT-US-011 ;  
 TELECOMMUNICATION INFORMATION: ;  
 TELEPHONE: 713-482-2961 ;  
 TELEFAX: 713-663-7290 ;  
 TELEX: ;  
 INFORMATION FOR SEQ ID NO: 2: ;  
 SEQUENCE CHARACTERISTICS: ;  
 LENGTH: 10 ;  
 TYPE: AMINO ACID ;  
 STRANDBNESS: SINGLE ;  
 TOPOLOGY: LINEAR ;  
 MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 2 ;  
 HYPOTHICAL: NO ;  
 ANTI-SENSE: NO ;  
 FRAGMENT TYPE: N ;  
 ORIGINAL SOURCE: SYNTHETIC ;  
 US-08-657-163A-2 ;

Query Match 78.3%; Score 54; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; ;  
 Qy 1 ||||||| LKAMDPPTPL 10  
 Db 1 LKAMDPPTPL 10

RESULT 4  
 US-09-134-000C-5938  
 ; Sequence 5938, Application US/09134000C  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 032796-032  
 ; CURRENT APPLICATION NUMBER: US/09/134,000C  
 ; CURRENT FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/055,778  
 ; PRIOR FILING DATE: 1997-08-15  
 ; NUMBER OF SEQ ID NOS: 6812  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 5938  
 ; LENGTH: 137  
 ; TYPE: PRT  
 ; ORGANISM: Enterococcus faecalis  
 US-09-134-000C-5938

Query Match 65.2%; Score 45; DB 4; Length 137;  
 Best Local Similarity 75.0%; Pred. No. 4.7; Mismatches 2; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DPTPPLWI 12  
 Db 85 :|||||: NPPPLWV 92

RESULT 5  
 US-08-188-592-20  
 ; Sequence 20, Application US/08188592  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tjian, Robert  
 ; APPLICANT: Comai, Lucio  
 ; APPLICANT: Dynact, Brian D.  
 ; APPLICANT: Hoey, Timothy  
 ; APPLICANT: Ruppert, Siegfried  
 ; APPLICANT: Tanese, Naoko  
 ; APPLICANT: Wang, Edith  
 ; APPLICANT: Weinzierl, Robert O.J.  
 ; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, METHODS OF USE  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FLIEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94114-1487  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; ZIP: 94114-1487  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; REFERENCE/DOCKET NUMBER: A-57650-2/AUT/RAO  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEX: (415) 398-3249  
 ; FILING DATE: 28-JAN-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Osman, Richard A  
 ; REGISTRATION NUMBER: 36,627  
 ; REFERENCE/DOCKET NUMBER: A-57650-2/AUT/RAO  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1213 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-188-592-20

Query Match 62.3%; Score 43; DB 1; Length 1213;  
 Best Local Similarity 66.7%; Pred. No. 1e+02; Mismatches 8; Indels 1; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 |||| :||||| LKAMDPPTPLI 12  
 Db 620 LSAMDDSPVLWI 631

RESULT 6  
 US-08-646-715-20  
 ; Sequence 20, Application US/08646715  
 ; PATENT NO. 5637686  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tjian, Robert  
 ; APPLICANT: Comai, Lucio  
 ; APPLICANT: Dynact, Brian D.  
 ; APPLICANT: Hoey, Timothy  
 ; APPLICANT: Ruppert, Siegfried  
 ; APPLICANT: Tanese, Naoko  
 ; APPLICANT: Wang, Edith  
 ; APPLICANT: Weinzierl, Robert O.J.  
 ; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, METHODS OF USE  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FLIEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94114-1487  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,715  
 FILING DATE: 09-MAY-1996  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/188,582  
 FILING DATE: 28-JAN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Osman, Richard A.  
 REFERENCE NUMBER: 36,627  
 DOCKET NUMBER: A-57650-2/AJT/RAO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEX: 910 27299  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQENCE CHARACTERISTICS:  
 LENGTH: 1213 amino acids  
 TYPE: amino acid  
 MOLECULE TYPE: protein  
 US-08-646-715-20

Query Match 62.3%; Score 43; DB 1; Length 1213;  
 Best Local Similarity 66.7%; Pred. No. 1e+02; 1; Mismatches 3; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	1	1KAMDPTPPW1	12	:	620	ISAMDDSPVWI	631
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Db

RESULT 7  
 US-10-140-002-482  
 ; Sequence 482, Application US/10140002  
 ; Patent No. 6725730  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Denoyer, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary B.  
 ; APPLICANT: Godowski, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3330R1C59  
 ; CURRENT APPLICATION NUMBER: US/10/140,002  
 ; CURRENT FILING DATE: 2002-05-06  
 ; Prior Application removed - See Palm or File Wrapper  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 482  
 ; LENGTH: 212  
 ; ORGANISM: Homo Sapien  
 ; TYPE: PRT  
 ; US-10-140-002-482

Query Match 59.4%; Score 41; DB 4; Length 212;  
 Best Local Similarity 66.7%; Pred. No. 33; 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; Mismatches 1;

Qy	1	1KAMDPTPPW1	11	:	70	IKAVSPSPNW1	80
----	---	-------------	----	---	----	-------------	----

Db

RESULT 8  
 US-09-270-767-43223  
 ; Sequence 43223, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7226-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 43223  
 ; LENGTH: 253  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; FEATURE:  
 ; OTHER INFORMATION: Xaa means any amino acid  
 ; US-09-270-767-43223

Query Match 59.4%; Score 41; DB 4; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 40; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	4	MDPTPFL	10		43	MDPTPFL	49
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Db

RESULT 9  
 US-09-270-767-57545  
 ; Sequence 57545, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7226-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 57545  
 ; LENGTH: 198  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; FEATURE:  
 ; OTHER INFORMATION: Xaa means any amino acid  
 ; US-09-270-767-57545

Query Match 58.0%; Score 40; DB 4; Length 198;  
 Best Local Similarity 54.5%; Pred. No. 44; 2; Indels 0; Gaps 0;  
 Matches 6; Conservative 3; Mismatches 2;

Qy	1	1KAMDPTPPW1	11	:	70	IKAVSPSPNW1	80
----	---	-------------	----	---	----	-------------	----

Db

RESULT 10  
 US-09-270-767-42265  
 ; Sequence 42265, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7226-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517

! SOFTWARE: PatentIn Ver. 2.0  
! SEQ ID NO: 42265  
! LENGTH: 360  
! TYPE: PRT  
! ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-42265

Query Match 58.0%; Score 40; DB 4; Length 360;  
Best Local Similarity 54.5%; Pred. No. 84;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 LKAMDPTPLW 11  
Db 70 IKAVSPSPNLW 80

RESULT 11  
US-08-477-396A-1B  
Sequence 18, Application US/08477396A  
Patent No. 587235  
GENERAL INFORMATION:  
APPLICANT: Chen, Lan Bo  
APPLICANT: Bao, Shideng  
APPLICANT: Liu, Yuan  
TITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF ISOLATING SAME  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weingarten, Schurigin, Gagnebin & Hayes  
STREET: Ten Post Office Square  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,396A  
FILING DATE: 28-MAY-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,488  
FILING DATE: 29-OCT-1994  
APPLICATION NUMBER: US 08/448,388  
FILING DATE: 28-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/12502  
FILING DATE: 31-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Heine, Holliday C.  
REGISTRATION NUMBER: 34,346  
REFERENCE/DOCKET NUMBER: DFCL-333BX

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-2290  
TELEFAX: (617) 451-0313  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 206 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-477-396A-1B

Query Match 56.5%; Score 39; DB 4; Length 210;  
Best Local Similarity 60.0%; Pred. No. 69;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 KAMDPTPLW 11  
Db 134 KSDDPTNPW 143

RESULT 12  
US-09-270-767-45215  
Sequence 45215, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Hamburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SEQ ID NO 45215  
LENGTH: 210  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-45215

Query Match 56.5%; Score 39; DB 4; Length 210;  
Best Local Similarity 66.7%; Pred. No. 67;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 MDPPMPPLW 12  
Db 82 LDGNNPPLW 90

RESULT 13  
US-07-857-224B-42  
Sequence 42, Application US/07857224B  
Patent No. 595878  
GENERAL INFORMATION:  
APPLICANT: Benner, Steven A.  
TITLE OF INVENTION: Predicting Folded Structures of Proteins  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Steven A. Benner  
STREET: Hadlaubstrasse 151  
CITY: Zurich  
STATE: none  
COUNTRY: Switzerland  
ZIP: (note: this is an international post code) CH-8092

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
FILING DATE: 03/25/92  
CLASSIFICATION: 436  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/07/857,224B  
FILING DATE: 03/25/92  
CLASSIFICATION: 436  
PRIORITY APPLICATION DATA: none  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (International) 41 1 632 2830  
TELEFAX: (International) 41 1 262 2437  
TELEX: none  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
ORIGINAL SOURCE: protein  
ORGANISM: Saccharomyces cerevisiae

FEATURE: Protein kinase; Table 8 Column 48  
 PUBLICATION INFORMATION:  
 AUTHORS: Hanks, S. K.  
 AUTHORS: Quinn, A. M.  
 AUTHORS: Hunter, T.  
 TITLE: The protein kinase family  
 JOURNAL: Science  
 VOLUME: 241  
 PAGES: 42-52  
 DATE: 1988  
 US-07-857-224B-42

Query Match 55.1%; Score 38; DB 2; Length 267;  
 Best Local Similarity 70.0%; Pred. No. 1.3e+02; 2; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 0; Db

Qy 1 LKAMDPTPP 10  
 ||||| :||| 31 LRVNDPTPEL 40

RESULT 14  
 US-09-377-285B-40  
 Sequence 40; Application US/09377285B  
 Patent No. 6720175  
 GENERAL INFORMATION:  
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
 APPLICANT: WORLBY, Paul  
 APPLICANT: TU, Jian  
 APPLICANT: XIAO, Bo  
 APPLICANT: LEAHY, Daniel  
 APPLICANT: BENKELEN, Jutta  
 APPLICANT: LANHAM, Anthony  
 TITLE OF INVENTION: NUCLEAR ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)  
 FILE REFERENCE: JHU1580-4  
 CURRENT APPLICATION NUMBER: US/09/377,285B  
 CURRENT FILING DATE: 1999-08-18  
 PRIOR APPLICATION NUMBER: US 60/138,426  
 PRIOR FILING DATE: 1999-05-10  
 PRIOR APPLICATION NUMBER: US 60/138,493  
 PRIOR FILING DATE: 1999-06-10  
 PRIOR APPLICATION NUMBER: US 60/138,494  
 PRIOR FILING DATE: 1999-06-10  
 PRIOR APPLICATION NUMBER: US 60/097,334  
 PRIOR FILING DATE: 1998-08-18  
 NUMBER OF SEQ ID NOS: 72  
 SOFTWARE: Patentin version 3.0  
 SEQ ID NO: 40  
 LENGTH: 1740  
 TYPE: PRT  
 ORGANISM: Rattus norvegicus  
 US-09-377-285B-40

RESULT 15  
 US-08-602-999A-444  
 Sequence 444; Application US/08602999A  
 Patent No. 618405  
 GENERAL INFORMATION:  
 APPLICANT: SPARKS, Andrew B.  
 APPLICANT: KAY, Brian K.  
 APPLICANT: THORN, Judith M.  
 APPLICANT: OULLIUM, Lawrence A.  
 APPLICANT: DBR, Channing J.

Query Match 55.1%; Score 38; DB 4; Length 1740;  
 Best Local Similarity 62.5%; Pred. No. 9.5e+02; 2; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 2; Db

Qy 4 MDPPPLW 11  
 ||||| :||| 26 LDPTAPVW 33

Search completed: January 6, 2005, 10:25:07  
 Job time: 25.3243 Secs

US-08-602-999A-444

Query Match 53.6%; Score 37; DB 3; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 8.6; 2; Mismatches 1; Indels 0; Gaps 0;  
 Matches 6; Conservative 2; Db

Qy 2 KAMDPPTPL 10  
 ||||| :||| 5 RAUPPTPPL 13